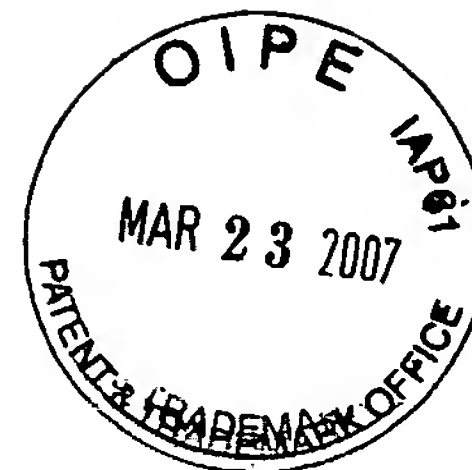


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SEQUENCE LISTING



<110> Lanahan, Mike

<120> self-processing Plants and Plant Parts

<130> 109846.317

<140> PCT/US04/07182

<141> 2004-03-15

<160> 112

<170> FastSEQ for Windows Version 4.0

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<211> 436

<212> PRT

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Arg	Ala	Gly	Gly	Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Gly	Asp	Tyr	Thr	115	120	125	
Trp	Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	130	135	140	
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Val	Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	210	215	220	
Trp	Asp	Thr	Asn	Val	Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Gly	225	230	235	240
Ala	Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala	Ala	Phe	245	250	255	
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Thr	Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val	Ala	Asn	275	280	285	
His	Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	Phe	Ile	290	295	300	

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Leu	Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Tyr	Asp	Ser	Asp	Glu	Met
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Ile	Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile	Thr	Tyr
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Ile	Asn	Leu	Gly	Ser	Ser	Lys	Val	Gly	Arg	Trp	Val	Tyr	Val	Pro	Lys
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Val	Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu	Ala	Pro
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Ala	Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp	Ser	Tyr
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Phe	Leu	Thr	Asn	Pro	Val	Asp	Thr	Lys	Lys	Lys	Glu	Leu	Phe	Lys	Val
			100					105					110		
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		115					120					125			
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Phe	Glu	Lys	Tyr	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Tyr	Leu	Phe	Met	Val
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Arg	Glu	Val	Lys	Glu	Met	Val	Lys	Ala	Leu	His	Lys	His	Gly	Ile	Gly
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Val	Lys	Glu	Tyr	His	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Gln	Met	Gly	Leu
				485					490					495	
Ile	Asp	Lys	Lys	Thr	Met	Leu	Glu	Val	Glu	Arg	Ala	Leu	His	Lys	Ile
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			580					585					590			
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		595					600					605				
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	610					615					620					
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<211> 693

<212> PRT

<213> Sulfolobus solfataricus

<400> 5

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Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile Val Gln Gln
      35      40      45
Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys Glu His Ile
      50      55      60
Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys Arg Lys Arg
      65      70      75      80
Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys Tyr Gln Asp
      85      90      95
Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys Asp Gly Val
      100      105      110
Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile Phe Asp Val
      115      120      125
Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro Glu Asp Ser
      130      135      140
Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp Val Leu Glu
      145      150      155      160
Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro Met Trp Ala
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Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln Asp Lys Val
      180      185      190
Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg Val Ala Gly
      195      200      205
Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu Phe Thr Trp
      210      215      220
His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp Glu Leu His
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Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu	Trp	Trp	Ala	Gly
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Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly	Ile	Trp	Leu	Asp
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Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala	Met	Ala	Thr	Phe
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Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu	Gln	Leu	Val	Leu
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Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe	Leu	Pro	Asp	Tyr
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Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu	Pro	Arg	Gly	Lys
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625					630				635						640
Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr	Ser	Glu	Lys	Pro
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Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile	Gln	Val	Glu	Lys
			660					665					670		
Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln	Lys	Ile	Arg	Gly
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<210> 6

<211> 2082

<212> DNA

<213> Sulfolobus solfataricus

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<400> 6

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atcgtggacg	actccaagga	gatccaggtg	gagaagacca	tgcagaacac	ctacgtggcc	2040
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<210> 7

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 7

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gcggacacgc	tcagcatgcg	gaccagcgcg	cgcgcggcgc	ccaggcacca	gcaccagcag	180
gcgcgccgcg	gggcccaggtt	cccgtcgtc	gtcgtgtgcg	ccagcgccgg	catgaacgtc	240
gtcttcgtcg	gcgcccagat	ggcgccgtgg	agcaagaccg	gaggcctcgg	cgacgtcctc	300
ggcggcctgc	cgccggccat	ggccgcgaac	gggcaccgtg	tcatggtcgt	ctctccccgc	360
tacgaccagt	acaaggacgc	ctgggacacc	agcgtcgtgt	ccgagatcaa	gatgggagac	420
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gaccacccac	tgttcctgga	gagggtttgg	ggaaagaccg	aggagaagat	ctacgggcct	540
gtcgttgga	cggactacag	ggacaaccag	ctgcggttca	gcctgctatg	ccaggcagca	600
cttgaagctc	caaggatcct	gagcctcaac	aacaacccat	acttctccgg	accatacggg	660
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<210> 8

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 8

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Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg Thr
 35          40          45
Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg Gly
 50          55          60
Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Met Asn Val
 65          70          75          80
Val Phe Val Gly Ala Glu Met Ala Pro Trp Ser Lys Thr Gly Gly Leu
          85          90          95
Gly Asp Val Leu Gly Gly Leu Pro Pro Ala Met Ala Ala Asn Gly His
 100          105          110
Arg Val Met Val Val Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp
 115          120          125
Asp Thr Ser Val Val Ser Glu Ile Lys Met Gly Asp Gly Tyr Glu Thr
 130          135          140
Val Arg Phe Phe His Cys Tyr Lys Arg Gly Val Asp Arg Val Phe Val
 145          150          155          160
Asp His Pro Leu Phe Leu Glu Arg Val Trp Gly Lys Thr Glu Glu Lys
          165          170          175
Ile Tyr Gly Pro Val Ala Gly Thr Asp Tyr Arg Asp Asn Gln Leu Arg
 180          185          190
Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu Ala Pro Arg Ile Leu Ser
 195          200          205
Leu Asn Asn Asn Pro Tyr Phe Ser Gly Pro Tyr Gly Glu Asp Val Val
 210          215          220
Phe Val Cys Asn Asp Trp His Thr Gly Pro Leu Ser Cys Tyr Leu Lys
 225          230          235          240
Ser Asn Tyr Gln Ser His Gly Ile Tyr Arg Asp Ala Lys Thr Ala Phe
          245          250          255
Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe Ser Asp Tyr
 260          265          270
Pro Glu Leu Asn Leu Pro Glu Arg Phe Lys Ser Ser Phe Asp Phe Ile
 275          280          285
Asp Gly Tyr Glu Lys Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys
 290          295          300
Ala Gly Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr

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305	Ala	Glu	Glu	Leu	Ile	310	Ser	Gly	Ile	Ala	Arg	315	Gly	Cys	Glu	Leu	Asp	320	Asn
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	Ser	Glu	Trp	Asp	Pro	Ser	Arg	Asp	Lys	Tyr	Ile		Ala	Val	Lys	Tyr	Asp		
			355					360							365				
	Val	Ser	Thr	Ala	Val	Glu	Ala	Lys	Ala	Leu	Asn		Lys	Glu	Ala	Leu	Gln		
		370					375						380						
	Ala	Glu	Val	Gly	Leu	Pro	Val	Asp	Arg	Asn	Ile		Pro	Leu	Val	Ala	Phe		
385						390					395						400		
	Ile	Gly	Arg	Leu	Glu	Gln	Lys	Gly	Pro	Asp	Val	Met	Ala	Ala	Ala				
				405						410					415				
	Ile	Pro	Gln	Leu	Met	Glu	Met	Val	Glu	Asp	Val	Gln	Ile	Val	Leu	Leu			
				420					425					430					
	Gly	Thr	Gly	Lys	Lys	Lys	Phe	Glu	Arg	Met	Leu	Met	Ser	Ala	Glu	Glu			
			435					440					445						
	Lys	Phe	Pro	Gly	Lys	Val	Arg	Ala	Val	Val	Lys	Phe	Asn	Ala	Ala	Leu			
		450					455					460							
	Ala	His	His	Ile	Met	Ala	Gly	Ala	Asp	Val	Leu	Ala	Val	Thr	Ser	Arg			
465						470					475					480			
	Phe	Glu	Pro	Cys	Gly	Leu	Ile	Gln	Leu	Gln	Gly	Met	Arg	Tyr	Gly	Thr			
				485						490					495				
	Pro	Cys	Ala	Cys	Ala	Ser	Thr	Gly	Gly	Leu	Val	Asp	Thr	Ile	Ile	Glu			
				500					505					510					
	Gly	Lys	Thr	Gly	Phe	His	Met	Gly	Arg	Leu	Ser	Val	Asp	Cys	Asn	Val			
			515					520					525						
	Val	Glu	Pro	Ala	Asp	Val	Lys	Val	Ala	Thr	Thr	Leu	Gln	Arg	Ala				
		530					535					540							
	Ile	Lys	Val	Val	Gly	Thr	Pro	Ala	Tyr	Glu	Glu	Met	Val	Arg	Asn	Cys			
545						550				555					560				
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				565					570					575					
	Val	Leu	Leu	Ser	Leu	Gly	Val	Ala	Gly	Gly	Glu	Pro	Gly	Val	Glu	Gly			
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<210> 9
 <211> 2223
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 9

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<210> 10

<211> 741

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 10

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Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
35     40     45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
50     55     60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65     70     75     80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
85     90     95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
100    105    110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
115    120    125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
130    135    140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145    150    155    160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
165    170    175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
180    185    190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
195    200    205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
210    215    220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225    230    235    240

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Thr	Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val	Ala	Asn	
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His	Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	Phe	Ile	
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Leu	Thr	Tyr	Glu	Gly	Gln	Pro	Thr	Ile	Phe	Tyr	Arg	Asp	Tyr	Glu	Glu	
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Trp	Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His	Asp	Asn	
				325					330					335		
Leu	Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Tyr	Asp	Ser	Asp	Glu	Met	
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Ile	Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile	Thr	Tyr	
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Phe	Ala	Gly	Ala	Cys	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly	Gly	Trp	
385					390					395					400	
Val	Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu	Ala	Pro	
				405					410					415		
Ala	Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp	Ser	Tyr	
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Cys	Gly	Val	Gly	Thr	Ser	Ile	Ala	Gly	Ile	Leu	Glu	Ala	Asp	Arg	Val	
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Leu	Thr	Val	Ser	Pro	Tyr	Tyr	Ala	Glu	Glu	Leu	Ile	Ser	Gly	Ile	Ala	
	450					455					460					
Arg	Gly	Cys	Glu	Leu	Asp	Asn	Ile	Met	Arg	Leu	Thr	Gly	Ile	Thr	Gly	
465					470					475					480	
Ile	Val	Asn	Gly	Met	Asp	Val	Ser	Glu	Trp	Asp	Pro	Ser	Arg	Asp	Lys	
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Tyr	Ile	Ala	Val	Lys	Tyr	Asp	Val	Ser	Thr	Ala	Val	Glu	Ala	Lys	Ala	
			500					505					510			
Leu	Asn	Lys	Glu	Ala	Leu	Gln	Ala	Glu	Val	Gly	Leu	Pro	Val	Asp	Arg	
		515					520					525				
Asn	Ile	Pro	Leu	Val	Ala	Phe	Ile	Gly	Arg	Leu	Glu	Glu	Gln	Lys	Gly	
	530					535					540					
Pro	Asp	Val	Met	Ala	Ala	Ala	Ile	Pro	Gln	Leu	Met	Glu	Met	Val	Glu	
545					550					555					560	
Asp	Val	Gln	Ile	Val	Leu	Leu	Gly	Thr	Gly	Lys	Lys	Lys	Phe	Glu	Arg	
				565					570					575		
Met	Leu	Met	Ser	Ala	Glu	Glu	Lys	Phe	Pro	Gly	Lys	Val	Arg	Ala	Val	
			580					585					590			
Val	Lys	Phe	Asn	Ala	Ala	Leu	Ala	His	His	Ile	Met	Ala	Gly	Ala	Asp	
		595					600					605				
Val	Leu	Ala	Val	Thr	Ser	Arg	Phe	Glu	Pro	Cys	Gly	Leu	Ile	Gln	Leu	
	610					615					620					
Gln	Gly	Met	Arg	Tyr	Gly	Thr	Pro	Cys	Ala	Cys	Ala	Ser	Thr	Gly	Gly	
625					630					635					640	
Leu	Val	Asp	Thr	Ile	Ile	Glu	Gly	Lys	Thr	Gly	Phe	His	Met	Gly	Arg	
				645					650					655		
Leu	Ser	Val	Asp	Cys	Asn	Val	Val	Glu	Pro	Ala	Asp	Val	Lys	Lys	Val	
			660					665					670			
Ala	Thr	Thr	Leu	Gln	Arg	Ala	Ile	Lys	Val	Val	Gly	Thr	Pro	Ala	Tyr	
		675					680					685				
Glu	Glu	Met	Val	Arg	Asn	Cys	Met	Ile	Gln	Asp	Leu	Ser	Trp	Lys	Gly	
	690					695					700					
Pro	Ala	Lys	Asn	Trp	Glu	Asn	Val	Leu	Leu	Ser	Leu	Gly	Val	Ala	Gly	
705					710					715					720	
Gly	Glu	Pro	Gly	Val	Glu	Gly	Glu	Glu	Ile	Ala	Pro	Leu	Ala	Lys	Glu	
				725					730					735		
Asn	Val	Ala	Ala	Pro												

740

<210> 11
 <211> 1515
 <212> DNA
 <213> Zea mays

<400> 11
 ggagagctat gagacgtatg tcctcaaagc cactttgcat tgtgtgaaac caatatcgat 60
 ctttgttact tcatcatgca tgaacatttg tggaaactac tagcttaca gcattagtga 120
 cagctcagaa aaaagttatc tatgaaagg ttcattgtga ccgtgggaaa tgagaaatgt 180
 tgccaactca aacaccttca atatgttggt tgcaggcaaa ctcttctgga agaaagggtgt 240
 ctaaaactat gaacgggtta cagaaaggta taaaccacgg ctgtgcattt tgggaagtatc 300
 atctatagat gtctgttgag gggaaagccg tacgccaacg ttattttactc agaaacagct 360
 tcaacacaca gttgtctgct ttatgatggc atctccaccc aggcacccac catcacctat 420
 ctctcgtgcc tgtttatttt cttgcccttt ctgatcataa aaaaacatta agagtttgca 480
 aacatgcata ggcataatcaa tatgctcatt tattaatttg ctagcagatc atcttcctac 540
 tctttacttt atttattggt tgaaaaatat gtcctgcacc tagggagctc gtatacagta 600
 ccaatgcatc ttcattaaat gtgaatttca gaaaggaagt aggaacctat gagagtattt 660
 ttcaaaatta attagcggct tctattatgt ttatagcaaa ggccaagggtc aaaattggaa 720
 cactaatgat ggttggttgc atgagtctgt cgattacttg caagaaatgt gaacctttgt 780
 ttctgtgctg gggcataaaa caaacagctt ctagcctctt ttacggtact tgcacttgca 840
 agaaatgtga actccttttc atttctgtat gtggacataa tgccaaagca tccaggcttt 900
 ttcattggtg ttgatgtctt tacacagttc atctccacca gtatgccctc ctcatactct 960
 atataaacac atcaacagca tcgcaattag ccacaagatc acttcgggag gcaagtgcga 1020
 tttcgatctc gcagccacct ttttttggtc tgttgtaagt ataccttccc ttaccatctt 1080
 tatctgttag ttttaattgt aattgggaag tattagtga aagaggatga gatgctatca 1140
 tctatgtact ctgcaaatgc atctgacgtt atatgggctg cttcatataa tttgaattgc 1200
 tccattcttg ccgacaatat attgcaagggt atatgcctag ttccatcaaa agttctgttt 1260
 tttcatttca aaagcatttt agtggcacac aattttttgtc catgagggaa aggaaatctg 1320
 ttttggttac tttgcttgag gtgcattctt catatgtcca gttttatgga agtaataaac 1380
 ttcagtttgg tcataagatg tcatattaaa gggcaaacat atattcaatg ttcaattcat 1440
 cgtaaagtgt ccctttttgt aaaagattgc atactcattt atttgagttg cagggtgtatc 1500
 tagtagttgg aggag 1515

<210> 12
 <211> 673
 <212> DNA
 <213> Zea mays

<400> 12
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 ttggcatgta aagctccaag aatttggtgt atccttaaca actcacagaa catcaaccaa 120
 aattgcacgt caagggtatt gggtaagaaa caatcaaaca aatcctctct gtgtgcaaag 180
 aaacacggtg agtcatgccg agatcatact catctgatat acatgcttac agctcacaag 240
 acattacaaa caactcatat tgcattacaa agatcgtttc atgaaaaata aaataggccg 300
 gacaggacaa aaatccttga cgtgtaaagt aaatttacia caaaaaaaa gccatatgtc 360
 aagctaaatc taattcgttt tacgtagatc aacaacctgt agaaggcaac aaaactgagc 420
 cacgcagaag tacagaatga ttccagatga accatcgacg tgctacgtaa agagagtgc 480
 gagtcatata catttggtgaa gaaacatga agctgcctac agccgtctcg gtggcataag 540
 aacacaagaa attgtgttaa ttaatcaaag ctataaataa cgctcgcatg cctgtgcact 600
 tctccatcac caccactggg tcttcagacc attagcttta tctactccag agcgcagaag 660
 aacccgatcg aca 673

<210> 13
 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

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<400> 13

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
 20 25 30
 Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
 35 40 45
 Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
 50 55 60
 Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
 65 70 75 80
 Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
 85 90 95
 Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
 100 105 110
 Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
 115 120 125
 Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
 130 135 140
 Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
 145 150 155 160
 Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
 165 170 175
 Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
 180 185 190
 Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
 195 200 205
 Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
 210 215 220
 Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
 225 230 235 240
 Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
 245 250 255
 Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
 260 265 270
 Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
 275 280 285
 Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
 290 295 300
 Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
 305 310 315 320
 Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
 325 330 335
 Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
 340 345 350
 Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
 355 360 365
 Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
 370 375 380
 Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
 385 390 395 400
 Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
 405 410 415
 Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
 420 425 430
 Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
 435 440 445
 Ser Tyr Cys Gly Val Gly
 450

<210> 14

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 14

Met	Arg	Val	Leu	Leu	Val	Ala	Leu	Ala	Leu	Leu	Ala	Leu	Ala	Ala	Ser
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Ala	Thr	Ser	Ala	Lys	Tyr	Leu	Glu	Leu	Glu	Glu	Gly	Gly	Val	Ile	Met
			20				25						30		
Gln	Ala	Phe	Tyr	Trp	Asp	Val	Pro	Ser	Gly	Gly	Ile	Trp	Trp	Asp	Thr
		35				40					45				
Ile	Arg	Gln	Lys	Ile	Pro	Glu	Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile
	50					55				60					
Trp	Ile	Pro	Pro	Ala	Ser	Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly
65					70				75						80
Tyr	Asp	Pro	Tyr	Asp	Tyr	Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly
				85					90					95	
Thr	Val	Glu	Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile
			100				105						110		
Asn	Thr	Ala	His	Ala	Tyr	Gly	Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile
		115				120						125			
Asn	His	Arg	Ala	Gly	Gly	Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Gly	Asp
	130					135					140				
Tyr	Thr	Trp	Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala
145					150					155					160
Asn	Tyr	Leu	Asp	Phe	His	Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly
				165					170					175	
Thr	Phe	Gly	Gly	Tyr	Pro	Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln
			180					185					190		
Tyr	Trp	Leu	Trp	Ala	Ser	Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser
		195					200					205			
Ile	Gly	Ile	Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala
	210					215					220				
Trp	Val	Val	Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly
225					230					235					240
Glu	Tyr	Trp	Asp	Thr	Asn	Val	Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Ser
				245					250					255	
Ser	Gly	Ala	Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala
			260					265					270		
Ala	Phe	Asp	Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn
		275					280					285			
Gly	Gly	Thr	Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val
	290					295					300				
Ala	Asn	His	Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala
305					310					315					320
Phe	Ile	Leu	Thr	Tyr	Glu	Gly	Gln	Pro	Thr	Ile	Phe	Tyr	Arg	Asp	Tyr
				325					330					335	
Glu	Glu	Trp	Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His
			340					345					350		
Asp	Asn	Leu	Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Tyr	Asp	Ser	Asp
		355					360					365			
Glu	Met	Ile	Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile
	370					375					380				
Thr	Tyr	Ile	Asn	Leu	Gly	Ser	Ser	Lys	Val	Gly	Arg	Trp	Val	Tyr	Val
385					390					395					400
Pro	Lys	Phe	Ala	Gly	Ala	Cys	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly
				405					410					415	
Gly	Trp	Val	Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu
			420					425					430		
Ala	Pro	Ala	Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp
		435					440					445			

Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
 450 455 460

<210> 15
 <211> 518
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 15
 Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
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 Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
 20 25 30
 Leu Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg
 35 40 45
 Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Ala Arg Arg
 50 55 60
 Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
 65 70 75 80
 Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala Phe
 85 90 95
 Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
 100 105 110
 Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro
 115 120 125
 Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro
 130 135 140
 Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu
 145 150 155 160
 Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala
 165 170 175
 His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg
 180 185 190
 Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp
 195 200 205
 Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
 210 215 220
 Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly
 225 230 235 240
 Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu
 245 250 255
 Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile
 260 265 270
 Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val
 275 280 285
 Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp
 290 295 300
 Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala
 305 310 315 320
 Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp
 325 330 335
 Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly Thr
 340 345 350
 Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His
 355 360 365
 Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu
 370 375 380
 Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp
 385 390 395 400

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Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu
 405 410 415
 Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile
 420 425 430
 Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile
 435 440 445
 Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys Phe
 450 455 460
 Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val
 465 470 475 480
 Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala
 485 490 495
 Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys
 500 505 510
 Gly Val Gly Thr Ser Ile
 515

<210> 16

<211> 820

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 16

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
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 Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
 20 25 30
 Leu Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg
 35 40 45
 Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
 50 55 60
 Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
 65 70 75 80
 Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala Phe
 85 90 95
 Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
 100 105 110
 Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro
 115 120 125
 Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro
 130 135 140
 Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu
 145 150 155 160
 Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala
 165 170 175
 His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg
 180 185 190
 Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp
 195 200 205
 Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
 210 215 220
 Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly
 225 230 235 240
 Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu
 245 250 255
 Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile
 260 265 270
 Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val
 275 280 285

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Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	Trp
	290					295					300				
Asp	Thr	Asn	Val	Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Gly	Ala
305					310					315					320
Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala	Ala	Phe	Asp
				325					330					335	
Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn	Gly	Gly	Thr
			340					345					350		
val	val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val	Ala	Asn	His
		355					360					365			
Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	Phe	Ile	Leu
370						375					380				
Thr	Tyr	Glu	Gly	Gln	Pro	Thr	Ile	Phe	Tyr	Arg	Asp	Tyr	Glu	Glu	Trp
385					390					395					400
Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His	Asp	Asn	Leu
				405					410					415	
Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Tyr	Asp	Ser	Asp	Glu	Met	Ile
			420					425					430		
Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile	Thr	Tyr	Ile
		435					440					445			
Asn	Leu	Gly	Ser	Ser	Lys	Val	Gly	Arg	Trp	Val	Tyr	Val	Pro	Lys	Phe
450						455					460				
Ala	Gly	Ala	Cys	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly	Gly	Trp	Val
465					470					475					480
Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu	Ala	Pro	Ala
				485					490					495	
Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp	Ser	Tyr	Cys
			500					505					510		
Gly	Val	Gly	Thr	Ser	Ile	Ala	Gly	Ile	Leu	Glu	Ala	Asp	Arg	Val	Leu
		515					520					525			
Thr	Val	Ser	Pro	Tyr	Tyr	Ala	Glu	Glu	Leu	Ile	Ser	Gly	Ile	Ala	Arg
530						535					540				
Gly	Cys	Glu	Leu	Asp	Asn	Ile	Met	Arg	Leu	Thr	Gly	Ile	Thr	Gly	Ile
545					550					555					560
Val	Asn	Gly	Met	Asp	Val	Ser	Glu	Trp	Asp	Pro	Ser	Arg	Asp	Lys	Tyr
				565					570					575	
Ile	Ala	Val	Lys	Tyr	Asp	Val	Ser	Thr	Ala	Val	Glu	Ala	Lys	Ala	Leu
			580					585					590		
Asn	Lys	Glu	Ala	Leu	Gln	Ala	Glu	Val	Gly	Leu	Pro	Val	Asp	Arg	Asn
		595					600					605			
Ile	Pro	Leu	Val	Ala	Phe	Ile	Gly	Arg	Leu	Glu	Glu	Gln	Lys	Gly	Pro
610						615					620				
Asp	Val	Met	Ala	Ala	Ala	Ile	Pro	Gln	Leu	Met	Glu	Met	Val	Glu	Asp
625					630					635					640
Val	Gln	Ile	Val	Leu	Gly	Thr	Gly	Lys	Lys	Lys	Lys	Phe	Glu	Arg	Met
				645				650						655	
Leu	Met	Ser	Ala	Glu	Glu	Lys	Phe	Pro	Gly	Lys	Val	Arg	Ala	Val	Val
			660					665					670		
Lys	Phe	Asn	Ala	Ala	Leu	Ala	His	His	Ile	Met	Ala	Gly	Ala	Asp	Val
		675					680					685			
Leu	Ala	Val	Thr	Ser	Arg	Phe	Glu	Pro	Cys	Gly	Leu	Ile	Gln	Leu	Gln
690						695					700				
Gly	Met	Arg	Tyr	Gly	Thr	Pro	Cys	Ala	Cys	Ala	Ser	Thr	Gly	Gly	Leu
705					710					715					720
Val	Asp	Thr	Ile	Ile	Glu	Gly	Lys	Thr	Gly	Phe	His	Met	Gly	Arg	Leu
				725					730					735	
Ser	Val	Asp	Cys	Asn	Val	Val	Glu	Pro	Ala	Asp	Val	Lys	Lys	Val	Ala
			740					745					750		
Thr	Thr	Leu	Gln	Arg	Ala	Ile	Lys	Val	Val	Gly	Thr	Pro	Ala	Tyr	Glu
		755					760					765			
Glu	Met	Val	Arg	Asn	Cys	Met	Ile	Gln	Asp	Leu	Ser	Trp	Lys	Gly	Pro
770						775					780				
Ala	Lys	Asn	Trp	Glu	Asn	Val	Leu	Leu	Ser	Leu	Gly	Val	Ala	Gly	Gly

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Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp	Leu	Leu	Leu
290						295					300				
Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Ile	Tyr	Asp	Thr	Thr	Leu
305					310					315					320
Ala	Met	Tyr	Glu	Val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys	Gly	Gly	Leu
				325					330					335	
Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val	Glu	Asp	Leu
			340					345					350		
Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu	Gly	Phe	Lys
		355					360					365			
Ile	Ala	Tyr	Lys	Leu	Ala	Lys	Asp	Gly	Val	Phe	Asp	Lys	Phe	Ile	Glu
370						375					380				
Glu	Lys	Tyr	Arg	Ser	Phe	Lys	Glu	Gly	Ile	Gly	Lys	Glu	Ile	Val	Glu
385					390					395					400
Gly	Lys	Thr	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile	Asp	Lys	Glu
				405				410						415	
Asp	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu	Ser	Leu	Leu
			420					425					430		
Asn	Ser	Tyr	Ile	Val	Lys	Thr	Ile	Ala	Glu	Leu	Arg				
		435					440								

<210> 19
 <211> 1335
 <212> DNA
 <213> Thermotoga maritima

<400> 19

atggccgagt	tcttcccgga	gatcccgaag	atccagttcg	agggcaagga	gtccaccaac	60
ccgctcgcct	tccgcttcta	cgacccgaac	gaggtgatcg	acggcaagcc	gctcaaggac	120
cacctcaagt	tctccgtggc	cttctggcac	accttcgtga	acgagggccg	cgacccgttc	180
ggcgacccga	ccgccgagcg	cccgtggaac	cgcttctccg	acccgatgga	caaggccttc	240
gcccgcgtgg	acgccctctt	cgagttctgc	gagaagctca	acatcgagta	cttctgcttc	300
cacgaccgcg	acatcgcccc	ggagggcaag	accctccgcg	agaccaacaa	gatcctcgac	360
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Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asp	Leu	Gly	Phe	Glu	Leu	Glu	Asn
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Glu	Lys	Tyr	Arg	Ser	Phe	Arg	Glu	Gly	Ile	Gly	Arg	Asp	Ile	Val	Glu
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Gly	Lys	Val	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile	Asp	Lys	Glu
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<211> 1335

<212> DNA

<213> Thermotoga neapolitana

<400> 21

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cacctcaagt	tctccgtggc	cttctggcac	accttcgtga	acgagggccg	cgaccggttc	180
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aaggtggtgg agcgcataca ggagcgcata aaggactcca acgtgaagct cctctggggc 420
accgccaacc tcttctccca cccgcgctac atgcacggcg ccgccaccac ctgctccgcc 480
gacgtgttcg cctacgccgc cgcccagggtg aagaaggccc tggagatcac caaggagctg 540
ggcggcgagg gctacgtgtt ctggggcggc cgcgagggtt acgagaccct cctcaacacc 600
gacctcggct tcgagctgga gaacctcgcc cgcttcctcc gcatggccgt ggactacgcc 660
aagcgcatac gcttcaccgg ccagttcctc atcgagccga agccgaagga gccgaccaag 720
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 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 22
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 <212> DNA
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<220>
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<400> 23
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 <213> Artificial Sequence

<220>
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 35 40 45
 Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
 50 55 60
 Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
 65 70 75 80
 Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
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Phe	Lys	Val	Thr	Val	Asp	Gly	Lys	Glu	Ile	Pro	Val	Ser	Arg	Val	Glu
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	145				150					155					160
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		355					360					365			
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	385				390					395					400
Phe	Met	Val	Pro	Glu	Gly	Arg	Tyr	Ser	Thr	Asp	Pro	Lys	Asn	Pro	His
				405					410					415	
Thr	Arg	Ile	Arg	Glu	Val	Lys	Glu	Met	Val	Lys	Ala	Leu	His	Lys	His
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Ile	Ala	Ser	Glu	Arg	Pro	Met	Met	Arg	Lys	Phe	Ile	Val	Asp	Thr	Val
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			500					505					510		
Met	Gly	Leu	Ile	Asp	Lys	Lys	Thr	Met	Leu	Glu	Val	Glu	Arg	Ala	Leu
		515					520					525			
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	530					535					540				
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Lys Ala Asp Lys Lys Lys	Glu Trp Thr Glu Glu	Glu Leu Lys Asn Ala
645	650	655
Gln Lys Leu Ala Gly Ala	Ile Leu Leu Thr Ser	Gln Gly Val Pro Phe
660	665	670
Leu His Gly Gly Gln Asp	Phe Cys Arg Thr Thr	Asn Phe Asn Asp Asn
675	680	685
Ser Tyr Asn Ala Pro Ile	Ser Ile Asn Gly Phe	Asp Tyr Glu Arg Lys
690	695	700
Leu Gln Phe Ile Asp Val	Phe Asn Tyr His Lys	Gly Leu Ile Lys Leu
705	710	715
Arg Lys Glu His Pro Ala	Phe Arg Leu Lys Asn	Ala Glu Glu Ile Lys
725	730	735
Lys His Leu Glu Phe Leu	Pro Gly Gly Arg Arg	Ile Val Ala Phe Met
740	745	750
Leu Lys Asp His Ala Gly	Gly Asp Pro Trp Lys	Asp Ile Val Val Ile
755	760	765
Tyr Asn Gly Asn Leu Glu	Lys Thr Thr Tyr Lys	Leu Pro Glu Gly Lys
770	775	780
Trp Asn Val Val Val Asn	Ser Gln Lys Ala Gly	Thr Glu Val Ile Glu
785	790	795
Thr Val Glu Gly Thr Ile	Glu Leu Asp Pro Leu	Ser Ala Tyr Val Leu
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<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 25

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<211> 718

<212> PRT

<213> Artificial Sequence

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<400> 26

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Glu	His	Ile	Ile	Gly	Leu	Gly	Glu	Lys	Ala	Phe	Glu	Leu	Asp	Arg	Lys
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Val	Ala	Gly	Val	Phe	Leu	Asp	Ile	His	Tyr	Met	Asp	Ser	Tyr	Lys	Leu
225				230					235					240	
Phe	Thr	Trp	His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile	Asp
			245						250					255	
Glu	Leu	His	Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His	Gly
			260				265						270		

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Ile	Arg	Val	Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly	Lys
		275					280					285			
Phe	Cys	Glu	Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp	Pro
	290					295					300				
Gly	Thr	Thr	Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu	Trp
305					310					315					320
Trp	Ala	Gly	Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly	Ile
				325					330					335	
Trp	Leu	Asp	Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu	Ile
			340					345					350		
Arg	Asp	Val	Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg	Leu
		355					360					365			
Val	Thr	Thr	Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys	Arg
	370					375					380				
Val	Lys	His	Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala	Met
385					390					395					400
Ala	Thr	Phe	Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe	Ile
				405					410					415	
Leu	Ser	Arg	Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile	Trp
			420				425						430		
Thr	Gly	Asp	Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu	Gln
		435					440					445			
Leu	Val	Leu	Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys	Asp
	450					455					460				
Ile	Gly	Gly	Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser	Met
465					470					475					480
Asp	Leu	Leu	Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe	Tyr
				485					490					495	
Arg	Ser	His	Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe	Leu
			500					505					510		
Pro	Asp	Tyr	Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	Val	Glu	Leu	Arg	Tyr
		515					520					525			
Lys	Phe	Leu	Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu	Lys
	530					535					540				
Gly	His	Pro	Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp	Asp
545					550					555					560
Asp	Met	Tyr	Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu	Leu
				565					570					575	
Tyr	Ala	Pro	Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu	Pro
			580					585					590		
Arg	Gly	Lys	Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly	Lys
		595					600					605			
Ser	Val	Val	Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu	Gly
	610					615					620				
Ser	Ile	Ile	Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu	Thr
625					630					635					640
Ser	Phe	Lys	Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Ser	Asn	Glu
				645					650					655	
Ile	Lys	Phe	Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr	Ser
			660					665					670		
Glu	Lys	Pro	Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile	Gln
		675					680					685			
Val	Glu	Lys	Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln	Lys
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Ile	Arg	Gly	Lys	Ile	Asn	Leu	Glu	Ser	Glu	Lys	Asp	Glu	Leu		
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<210> 27

<211> 712

<212> PRT

<213> Artificial Sequence

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<220>

<223> synthetic

<400> 27

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			20					25					30		
Lys	Val	Val	Ile	Gly	Glu	Pro	Phe	Pro	Pro	Ile	Glu	Phe	Pro	Leu	Glu
		35					40					45			
Gln	Lys	Ile	Ser	Ser	Asn	Lys	Ser	Leu	Ser	Glu	Leu	Gly	Leu	Thr	Ile
	50					55					60				
Val	Gln	Gln	Gly	Asn	Lys	Val	Ile	Val	Glu	Lys	Ser	Leu	Asp	Leu	Lys
65				70					75						80
Glu	His	Ile	Ile	Gly	Leu	Gly	Glu	Lys	Ala	Phe	Glu	Leu	Asp	Arg	Lys
			85						90					95	
Arg	Lys	Arg	Tyr	Val	Met	Tyr	Asn	Val	Asp	Ala	Gly	Ala	Tyr	Lys	Lys
			100					105					110		
Tyr	Gln	Asp	Pro	Leu	Tyr	Val	Ser	Ile	Pro	Leu	Phe	Ile	Ser	Val	Lys
		115					120					125			
Asp	Gly	Val	Ala	Thr	Gly	Tyr	Phe	Phe	Asn	Ser	Ala	Ser	Lys	Val	Ile
	130					135					140				
Phe	Asp	Val	Gly	Leu	Glu	Glu	Tyr	Asp	Lys	Val	Ile	Val	Thr	Ile	Pro
145				150					155						160
Glu	Asp	Ser	Val	Glu	Phe	Tyr	Val	Ile	Glu	Gly	Pro	Arg	Ile	Glu	Asp
			165						170					175	
Val	Leu	Glu	Lys	Tyr	Thr	Glu	Leu	Thr	Gly	Lys	Pro	Phe	Leu	Pro	Pro
			180					185					190		
Met	Trp	Ala	Phe	Gly	Tyr	Met	Ile	Ser	Arg	Tyr	Ser	Tyr	Tyr	Pro	Gln
		195					200					205			
Asp	Lys	Val	Val	Glu	Leu	Val	Asp	Ile	Met	Gln	Lys	Glu	Gly	Phe	Arg
	210					215					220				
Val	Ala	Gly	Val	Phe	Leu	Asp	Ile	His	Tyr	Met	Asp	Ser	Tyr	Lys	Leu
225				230					235						240
Phe	Thr	Trp	His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile	Asp
			245						250					255	
Glu	Leu	His	Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His	Gly
			260					265					270		
Ile	Arg	Val	Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly	Lys
		275					280					285			
Phe	Cys	Glu	Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp	Pro
	290					295					300				
Gly	Thr	Thr	Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu	Trp
305					310					315					320
Trp	Ala	Gly	Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly	Ile
			325						330					335	
Trp	Leu	Asp	Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu	Ile
			340					345					350		
Arg	Asp	Val	Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg	Leu
		355					360					365			
Val	Thr	Thr	Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys	Arg
	370					375					380				
Val	Lys	His	Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala	Met
385				390					395						400
Ala	Thr	Phe	Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe	Ile
			405						410					415	
Leu	Ser	Arg	Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile	Trp
			420					425					430		
Thr	Gly	Asp	Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu	Gln
		435					440					445			
Leu	Val	Leu	Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys	Asp
	450					455					460				
Ile	Gly	Gly	Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser	Met

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<210> 28
<211> 469
<212> PRT
<213> Artificial Sequence
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<220>
<223> synthetic

<400> 28

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Glu	Gly	Lys 35	Glu	Ser	Thr	Asn	Pro 40	Leu	Ala	Phe	Arg	Phe 45	Tyr	Asp	Pro
Asn 50	Glu	Val	Ile	Asp	Gly	Lys 55	Pro	Leu	Lys	Asp	His 60	Leu	Lys	Phe	Ser
Val 65	Ala	Phe	Trp	His	Thr 70	Phe	Val	Asn	Glu	Gly 75	Arg	Asp	Pro	Phe	Gly 80
Asp	Pro	Thr	Ala	Glu 85	Arg	Pro	Trp	Asn	Arg 90	Phe	Ser	Asp	Pro	Met 95	Asp
Lys	Ala	Phe	Ala 100	Arg	Val	Asp	Ala	Leu 105	Phe	Glu	Phe	Cys	Glu 110	Lys	Leu
Asn	Ile	Glu 115	Tyr	Phe	Cys	Phe	His 120	Asp	Arg	Asp	Ile	Ala 125	Pro	Glu	Gly
Lys	Thr 130	Leu	Arg	Glu	Thr	Asn 135	Lys	Ile	Leu	Asp	Lys 140	Val	Val	Glu	Arg
Ile 145	Lys	Glu	Arg	Met	Lys 150	Asp	Ser	Asn	Val	Lys 155	Leu	Leu	Trp	Gly	Thr 160
Ala	Asn	Leu	Phe	Ser	His	Pro	Arg	Tyr	Met	His	Gly	Ala	Ala	Thr	Thr

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				165				170					175				
Cys	Ser	Ala	Asp	Val	Phe	Ala	Tyr	Ala	Ala	Ala	Gln	Val	Lys	Lys	Ala		
			180					185					190				
Leu	Glu	Ile	Thr	Lys	Glu	Leu	Gly	Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly		
		195					200					205					
Gly	Arg	Glu	Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asp	Leu	Gly	Leu	Glu		
	210					215					220						
Leu	Glu	Asn	Leu	Ala	Arg	Phe	Leu	Arg	Met	Ala	Val	Glu	Tyr	Ala	Lys		
225					230					235					240		
Lys	Ile	Gly	Phe	Thr	Gly	Gln	Phe	Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu		
				245					250					255			
Pro	Thr	Lys	His	Gln	Tyr	Asp	Phe	Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe		
			260					265					270				
Leu	Lys	Asn	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala		
		275					280					285					
Asn	His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met		
	290					295					300						
Ala	Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp		
305					310					315					320		
Leu	Leu	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Ile	Tyr	Asp		
				325					330					335			
Thr	Thr	Leu	Ala	Met	Tyr	Glu	Val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys		
			340					345					350				
Gly	Gly	Leu	Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val		
		355					360					365					
Glu	Asp	Leu	Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu		
	370					375					380						
Gly	Phe	Lys	Ile	Ala	Tyr	Lys	Leu	Ala	Lys	Asp	Gly	Val	Phe	Asp	Lys		
385					390					395					400		
Phe	Ile	Glu	Glu	Lys	Tyr	Arg	Ser	Phe	Lys	Glu	Gly	Ile	Gly	Lys	Glu		
				405					410					415			
Ile	Val	Glu	Gly	Lys	Thr	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile		
			420					425					430				
Asp	Lys	Glu	Asp	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu		
		435					440					445					
Ser	Leu	Asn	Ser	Tyr	Ile	Val	Lys	Thr	Ile	Ala	Glu	Leu	Arg	Ser			
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Glu	Lys	Asp	Glu	Leu													
465																	

<210> 29

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 29

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Ala	Thr	Ser	Met	Ala	Glu	Phe	Phe	Pro	Glu	Ile	Pro	Lys	Val	Gln	Phe		
			20				25					30					
Glu	Gly	Lys	Glu	Ser	Thr	Asn	Pro	Leu	Ala	Phe	Lys	Phe	Tyr	Asp	Pro		
		35				40					45						
Glu	Glu	Ile	Ile	Asp	Gly	Lys	Pro	Leu	Lys	Asp	His	Leu	Lys	Phe	Ser		
	50					55					60						
Val	Ala	Phe	Trp	His	Thr	Phe	Val	Asn	Glu	Gly	Arg	Asp	Pro	Phe	Gly		
65					70				75						80		
Asp	Pro	Thr	Ala	Asp	Arg	Pro	Trp	Asn	Arg	Tyr	Thr	Asp	Pro	Met	Asp		
			85					90						95			
Lys	Ala	Phe	Ala	Arg	Val	Asp	Ala	Leu	Phe	Glu	Phe	Cys	Glu	Lys	Leu		

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Asn	Ile	Glu	100	Tyr	Phe	Cys	Phe	His	105	Asp	Arg	Asp	Ile	Ala	110	Pro	Glu	Gly
Lys	Thr	115	Leu	Arg	Glu	Thr	Asn	120	Lys	Ile	Leu	Asp	Lys	125	Val	Val	Glu	Arg
Ile	Lys	130	Glu	Arg	Met	Lys	135	Asp	Ser	Asn	Val	Lys	140	Leu	Leu	Trp	Gly	Thr
Ala	Asn	145	Leu	Phe	Ser	His	150	Pro	Arg	Tyr	Met	His	155	Gly	Ala	Ala	Thr	Thr
Cys	Ser	165	Ala	Asp	Val	Phe	Ala	Tyr	Ala	Ala	Ala	Gln	170	Val	Lys	Lys	Ala	
Leu	Glu	180	Ile	Thr	Lys	Glu	Leu	Gly	185	Gly	Glu	Gly	Tyr	190	Val	Phe	Trp	Gly
Gly	Arg	195	Glu	Gly	Tyr	Glu	Thr	Leu	200	Leu	Asn	Thr	Asp	205	Leu	Gly	Phe	Glu
Leu	Glu	210	Asn	Leu	Ala	Arg	Phe	Leu	215	Arg	Met	Ala	220	Val	Asp	Tyr	Ala	Lys
Arg	Ile	225	Gly	Phe	Thr	Gly	Gln	Phe	230	Leu	Ile	Glu	235	Pro	Lys	Pro	Lys	Glu
Pro	Thr	245	Lys	His	Gln	Tyr	Asp	Phe	250	Asp	Val	Ala	255	Thr	Ala	Tyr	Ala	Phe
Leu	Lys	260	Ser	His	Gly	Leu	Asp	Glu	265	Tyr	Phe	Lys	270	Phe	Asn	Ile	Glu	Ala
Asn	His	275	Ala	Thr	Leu	Ala	Gly	His	280	Thr	Phe	Gln	285	His	Glu	Leu	Arg	Met
Ala	Arg	290	Ile	Leu	Gly	Lys	Leu	Gly	295	Ser	Ile	Asp	300	Ala	Asn	Gln	Gly	Asp
Leu	Leu	305	Leu	Gly	Trp	Asp	Thr	Asp	310	Gln	Phe	Pro	315	Thr	Asn	Val	Tyr	Asp
Thr	Thr	325	Leu	Ala	Met	Tyr	Glu	Val	330	Ile	Lys	Ala	335	Gly	Gly	Phe	Thr	Lys
Gly	Gly	340	Leu	Asn	Phe	Asp	Ala	Lys	345	Val	Arg	Arg	350	Ala	Ser	Tyr	Lys	Val
Glu	Asp	355	Leu	Phe	Ile	Gly	His	Ile	360	Ala	Gly	Met	365	Asp	Thr	Phe	Ala	Leu
Gly	Phe	370	Lys	Val	Ala	Tyr	Lys	Leu	375	Val	Lys	Asp	380	Gly	Val	Leu	Asp	Lys
Phe	Ile	385	Glu	Glu	Lys	Tyr	Arg	Ser	390	Phe	Arg	Glu	395	Gly	Ile	Gly	Arg	Asp
Ile	Val	405	Glu	Gly	Lys	Val	Asp	Phe	410	Glu	Lys	Leu	415	Glu	Glu	Tyr	Ile	Ile
Asp	Lys	420	Glu	Thr	Ile	Glu	Leu	Pro	425	Ser	Gly	Lys	430	Gln	Glu	Tyr	Leu	Glu
Ser	Leu	435	Ile	Asn	Ser	Tyr	Ile	Val	440	Lys	Thr	Ile	445	Leu	Glu	Leu	Arg	Ser
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<210> 30

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 30

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			20					25					30		
Glu	Gly	Lys	Glu	Ser	Thr	Asn	Pro	Leu	Ala	Phe	Lys	Phe	Tyr	Asp	Pro

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		35				40				45					
Glu	Glu	Ile	Ile	Asp	Gly	Lys	Pro	Leu	Lys	Asp	His	Leu	Lys	Phe	Ser
50						55					60				
Val	Ala	Phe	Trp	His	Thr	Phe	Val	Asn	Glu	Gly	Arg	Asp	Pro	Phe	Gly
65					70					75					80
Asp	Pro	Thr	Ala	Asp	Arg	Pro	Trp	Asn	Arg	Tyr	Thr	Asp	Pro	Met	Asp
				85					90					95	
Lys	Ala	Phe	Ala	Arg	Val	Asp	Ala	Leu	Phe	Glu	Phe	Cys	Glu	Lys	Leu
			100					105					110		
Asn	Ile	Glu	Tyr	Phe	Cys	Phe	His	Asp	Arg	Asp	Ile	Ala	Pro	Glu	Gly
		115					120					125			
Lys	Thr	Leu	Arg	Glu	Thr	Asn	Lys	Ile	Leu	Asp	Lys	Val	Val	Glu	Arg
		130				135					140				
Ile	Lys	Glu	Arg	Met	Lys	Asp	Ser	Asn	Val	Lys	Leu	Leu	Trp	Gly	Thr
145					150					155					160
Ala	Asn	Leu	Phe	Ser	His	Pro	Arg	Tyr	Met	His	Gly	Ala	Ala	Thr	Thr
				165					170						
Cys	Ser	Ala	Asp	Val	Phe	Ala	Tyr	Ala	Ala	Ala	Gln	Val	Lys	Lys	Ala
			180					185					190		
Leu	Glu	Ile	Thr	Lys	Glu	Leu	Gly	Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly
		195					200					205			
Gly	Arg	Glu	Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asp	Leu	Gly	Phe	Glu
		210				215					220				
Leu	Glu	Asn	Leu	Ala	Arg	Phe	Leu	Arg	Met	Ala	Val	Asp	Tyr	Ala	Lys
225					230					235					240
Arg	Ile	Gly	Phe	Thr	Gly	Gln	Phe	Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu
				245					250					255	
Pro	Thr	Lys	His	Gln	Tyr	Asp	Phe	Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe
			260					265					270		
Leu	Lys	Ser	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala
		275					280					285			
Asn	His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met
		290				295					300				
Ala	Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp
305					310					315					320
Leu	Leu	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Val	Tyr	Asp
			325						330					335	
Thr	Thr	Leu	Ala	Met	Tyr	Glu	Val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys
			340					345					350		
Gly	Gly	Leu	Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val
		355					360					365			
Glu	Asp	Leu	Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu
		370				375					380				
Gly	Phe	Lys	Val	Ala	Tyr	Lys	Leu	Val	Lys	Asp	Gly	Val	Leu	Asp	Lys
385					390					395					400
Phe	Ile	Glu	Glu	Lys	Tyr	Arg	Ser	Phe	Arg	Glu	Gly	Ile	Gly	Arg	Asp
				405					410					415	
Ile	Val	Glu	Gly	Lys	Val	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile
			420					425					430		
Asp	Lys	Glu	Thr	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu
		435					440					445			
Ser	Leu	Ile	Asn	Ser	Tyr	Ile	Val	Lys	Thr	Ile	Leu	Glu	Leu	Arg	
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<211> 25

<212> PRT

<213> Artificial Sequence

<220>

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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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Met Gly Lys Asn Gly Asn Leu Cys Cys Phe Ser Leu Leu Leu Leu Leu
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 Leu Ala Gly Leu Ala Ser Gly His Gln
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<210> 32

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 32

Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
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 Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
 20 25 30

<210> 33

<211> 460

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<213> Artificial Sequence

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<223> synthetic

<400> 33

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
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 Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
 20 25 30
 Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
 35 40 45
 Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
 50 55 60
 Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
 65 70 75 80
 Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
 85 90 95
 Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
 100 105 110
 Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
 115 120 125
 Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
 130 135 140
 Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
 145 150 155 160
 Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
 165 170 175
 Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
 180 185 190
 Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
 195 200 205
 Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
 210 215 220
 Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
 225 230 235 240
 Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
 245 250 255

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Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
 260 265 270
 Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
 275 280 285
 Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
 290 295 300
 Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
 305 310 315 320
 Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
 325 330 335
 Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
 340 345 350
 Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
 355 360 365
 Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
 370 375 380
 Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
 385 390 395 400
 Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
 405 410 415
 Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
 420 425 430
 Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
 435 440 445
 Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
 450 455 460

<210> 34

<211> 825

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 34

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Ala Gly His Trp Tyr Lys His Gln Arg Ala Tyr Gln Phe
 20 25 30
 Thr Gly Glu Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met
 35 40 45
 Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
 50 55 60
 Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
 65 70 75 80
 Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
 85 90 95
 Asp Thr Ser Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val
 100 105 110
 Ile Glu Ala Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu
 115 120 125
 Phe Lys Val Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu
 130 135 140
 Lys Ala Asp Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val
 145 150 155 160
 Leu Ser Glu Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu
 165 170 175
 Ile Ile Glu Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu
 180 185 190
 Asp Asp Tyr Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu
 195 200 205

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Lys	Thr	Ile	Phe	Arg	Val	Trp	Ser	Pro	Val	Ser	Lys	Trp	Val	Lys	Val
210						215					220				
Leu	Leu	Phe	Lys	Asn	Gly	Glu	Asp	Thr	Glu	Pro	Tyr	Gln	Val	Val	Asn
225					230					235					240
Met	Glu	Tyr	Lys	Gly	Asn	Gly	Val	Trp	Glu	Ala	Val	Val	Glu	Gly	Asp
				245					250					255	
Leu	Asp	Gly	Val	Phe	Tyr	Leu	Tyr	Gln	Leu	Glu	Asn	Tyr	Gly	Lys	Ile
			260					265					270		
Arg	Thr	Thr	Val	Asp	Pro	Tyr	Ser	Lys	Ala	Val	Tyr	Ala	Asn	Asn	Gln
		275					280					285			
Glu	Ser	Ala	Val	Val	Asn	Leu	Ala	Arg	Thr	Asn	Pro	Glu	Gly	Trp	Glu
290						295					300				
Asn	Asp	Arg	Gly	Pro	Lys	Ile	Glu	Gly	Tyr	Glu	Asp	Ala	Ile	Ile	Tyr
305					310					315					320
Glu	Ile	His	Ile	Ala	Asp	Ile	Thr	Gly	Leu	Glu	Asn	Ser	Gly	Val	Lys
				325					330					335	
Asn	Lys	Gly	Leu	Tyr	Leu	Gly	Leu	Thr	Glu	Glu	Asn	Thr	Lys	Ala	Pro
			340					345					350		
Gly	Gly	Val	Thr	Thr	Gly	Leu	Ser	His	Leu	Val	Glu	Leu	Gly	Val	Thr
		355					360					365			
His	Val	His	Ile	Leu	Pro	Phe	Phe	Asp	Phe	Tyr	Thr	Gly	Asp	Glu	Leu
370						375					380				
Asp	Lys	Asp	Phe	Glu	Lys	Tyr	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Tyr	Leu
385					390					395					400
Phe	Met	Val	Pro	Glu	Gly	Arg	Tyr	Ser	Thr	Asp	Pro	Lys	Asn	Pro	His
				405					410					415	
Thr	Arg	Ile	Arg	Glu	Val	Lys	Glu	Met	Val	Lys	Ala	Leu	His	Lys	His
			420					425					430		
Gly	Ile	Gly	Val	Ile	Met	Asp	Met	Val	Phe	Pro	His	Thr	Tyr	Gly	Ile
		435					440					445			
Gly	Glu	Leu	Ser	Ala	Phe	Asp	Gln	Thr	Val	Pro	Tyr	Tyr	Phe	Tyr	Arg
450						455					460				
Ile	Asp	Lys	Thr	Gly	Ala	Tyr	Leu	Asn	Glu	Ser	Gly	Cys	Gly	Asn	Val
465					470					475					480
Ile	Ala	Ser	Glu	Arg	Pro	Met	Met	Arg	Lys	Phe	Ile	Val	Asp	Thr	Val
				485					490					495	
Thr	Tyr	Trp	Val	Lys	Glu	Tyr	His	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Gln
			500					505					510		
Met	Gly	Leu	Ile	Asp	Lys	Lys	Thr	Met	Leu	Glu	Val	Glu	Arg	Ala	Leu
		515					520					525			
His	Lys	Ile	Asp	Pro	Thr	Ile	Ile	Leu	Tyr	Gly	Glu	Pro	Trp	Gly	Gly
530						535					540				
Trp	Gly	Ala	Pro	Ile	Arg	Phe	Gly	Lys	Ser	Asp	Val	Ala	Gly	Thr	His
545					550					555					560
Val	Ala	Ala	Phe	Asn	Asp	Glu	Phe	Arg	Asp	Ala	Ile	Arg	Gly	Ser	Val
				565					570					575	
Phe	Asn	Pro	Ser	Val	Lys	Gly	Phe	Val	Met	Gly	Gly	Tyr	Gly	Lys	Glu
			580					585					590		
Thr	Lys	Ile	Lys	Arg	Gly	Val	Val	Gly	Ser	Ile	Asn	Tyr	Asp	Gly	Lys
		595					600					605			
Leu	Ile	Lys	Ser	Phe	Ala	Leu	Asp	Pro	Glu	Glu	Thr	Ile	Asn	Tyr	Ala
610						615					620				
Ala	Cys	His	Asp	Asn	His	Thr	Leu	Trp	Asp	Lys	Asn	Tyr	Leu	Ala	Ala
625					630					635					640
Lys	Ala	Asp	Lys	Lys	Lys	Glu	Trp	Thr	Glu	Glu	Glu	Leu	Lys	Asn	Ala
				645					650					655	
Gln	Lys	Leu	Ala	Gly	Ala	Ile	Leu	Leu	Thr	Ser	Gln	Gly	Val	Pro	Phe
			660					665					670		
Leu	His	Gly	Gly	Gln	Asp	Phe	Cys	Arg	Thr	Thr	Asn	Phe	Asn	Asp	Asn
		675					680					685			
Ser	Tyr	Asn	Ala	Pro	Ile	Ser	Ile	Asn	Gly	Phe	Asp	Tyr	Glu	Arg	Lys
690						695					700				
Leu	Gln	Phe	Ile	Asp	Val	Phe	Asn	Tyr	His	Lys	Gly	Leu	Ile	Lys	Leu

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705	Arg	Lys	Glu	His	Pro	710	Ala	Phe	Arg	Leu	Lys	715	Asn	Ala	Glu	Glu	Ile	720	Lys
					725						730							735	
	Lys	His	Leu	Glu	Phe	Leu	Pro	Gly	Gly	Arg	Arg	Ile	Val	Ala	Phe	Met			
			740						745					750					
	Leu	Lys	Asp	His	Ala	Gly	Gly	Asp	Pro	Trp	Lys	Asp	Ile	Val	Val	Ile			
			755					760					765						
	Tyr	Asn	Gly	Asn	Leu	Glu	Lys	Thr	Thr	Tyr	Lys	Leu	Pro	Glu	Gly	Lys			
			770				775					780							
	Trp	Asn	Val	Val	Val	Asn	Ser	Gln	Lys	Ala	Gly	Thr	Glu	Val	Ile	Glu			
						790					795					800			
	Thr	Val	Glu	Gly	Thr	Ile	Glu	Leu	Asp	Pro	Leu	Ser	Ala	Tyr	Val	Leu			
					805					810					815				
	Tyr	Arg	Glu	Ser	Glu	Lys	Asp	Glu	Leu										
			820						825										

<210> 35

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 35

Met	Arg	Val	Leu	Leu	Val	Ala	Leu	Ala	Leu	Leu	Ala	Leu	Ala	Ala	Ser				
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Ala	Thr	Ser	Ala	Lys	Tyr	Leu	Glu	Leu	Glu	Glu	Gly	Gly	Val	Ile	Met				
			20					25					30						
Gln	Ala	Phe	Tyr	Trp	Asp	Val	Pro	Ser	Gly	Gly	Ile	Trp	Trp	Asp	Thr				
		35					40					45							
Ile	Arg	Gln	Lys	Ile	Pro	Glu	Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile				
	50					55					60								
Trp	Ile	Pro	Pro	Ala	Ser	Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly				
65					70					75					80				
Tyr	Asp	Pro	Tyr	Asp	Tyr	Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly				
				85					90					95					
Thr	Val	Glu	Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile				
			100					105					110						
Asn	Thr	Ala	His	Ala	Tyr	Gly	Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile				
		115					120					125							
Asn	His	Arg	Ala	Gly	Gly	Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Gly	Asp				
		130				135					140								
Tyr	Thr	Trp	Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala				
145					150					155					160				
Asn	Tyr	Leu	Asp	Phe	His	Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly				
				165					170					175					
Thr	Phe	Gly	Gly	Tyr	Pro	Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln				
			180					185					190						
Tyr	Trp	Leu	Trp	Ala	Ser	Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser				
		195					200						205						
Ile	Gly	Ile	Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala				
	210					215					220								
Trp	Val	Val	Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly				
225					230					235					240				
Glu	Tyr	Trp	Asp	Thr	Asn	Val	Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Ser				
				245					250					255					
Ser	Gly	Ala	Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala				
			260					265					270						
Ala	Phe	Asp	Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn				
		275					280					285							
Gly	Gly	Thr	Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val				

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290	295	300														
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala																
305 Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr	310	315														320
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His	325	330														335
Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp	340	345														350
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile	355	360														365
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val	370	375														380
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly	385	390														395
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu	405	410														415
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp	420	425														430
Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu	435	440														445
	450	455														460

<210> 36

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 36

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser																
1 Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr	5	10														15
Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu	20	25														30
Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile	35	40														45
Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys	50	55														60
65 Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys	65	70														75
Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys	85	90														95
Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys	100	105														110
Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile	115	120														125
Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro	130	135														140
145 Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp	145	150														155
Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro	165	170														175
Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln	180	185														190
Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg	195	200														205
Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu	210	215														220
225 Phe Thr Trp His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp	225	230														235

60110USPCT1 Corrected SEQ LIST 2-2007.txt

				245					250					255			
Glu	Leu	His	Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His	Gly		
			260					265					270				
Ile	Arg	Val	Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly	Lys		
		275					280					285					
Phe	Cys	Glu	Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp	Pro		
	290					295					300						
Gly	Thr	Thr	Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu	Trp		
305					310					315					320		
Trp	Ala	Gly	Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly	Ile		
			325						330					335			
Trp	Leu	Asp	Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu	Ile		
			340					345					350				
Arg	Asp	Val	Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg	Leu		
		355					360					365					
Val	Thr	Thr	Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys	Arg		
	370					375					380						
Val	Lys	His	Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala	Met		
385					390					395					400		
Ala	Thr	Phe	Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe	Ile		
			405						410					415			
Leu	Ser	Arg	Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile	Trp		
			420					425					430				
Thr	Gly	Asp	Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu	Gln		
		435					440					445					
Leu	Val	Leu	Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys	Asp		
	450					455					460						
Ile	Gly	Gly	Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser	Met		
465					470					475					480		
Asp	Leu	Leu	Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe	Tyr		
			485					490					495				
Arg	Ser	His	Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe	Leu		
			500					505					510				
Pro	Asp	Tyr	Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	Val	Glu	Leu	Arg	Tyr		
		515					520					525					
Lys	Phe	Leu	Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu	Lys		
	530					535					540						
Gly	His	Pro	Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp	Asp		
545					550					555					560		
Asp	Met	Tyr	Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu	Leu		
			565					570						575			
Tyr	Ala	Pro	Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu	Pro		
			580					585					590				
Arg	Gly	Lys	Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly	Lys		
		595					600					605					
Ser	Val	Val	Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu	Gly		
	610					615					620						
Ser	Ile	Ile	Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu	Thr		
625					630					635					640		
Ser	Phe	Lys	Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Ser	Asn	Glu		
			645					650						655			
Ile	Lys	Phe	Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr	Ser		
			660					665					670				
Glu	Lys	Pro	Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile	Gln		
		675					680					685					
Val	Glu	Lys	Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln	Lys		
	690					695					700						
Ile	Arg	Gly	Lys	Ile	Asn	Leu	Glu	Ser	Glu	Lys	Asp	Glu	Leu				
705					710					715							

<210> 37
 <211> 1434

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<212> DNA

<213> *Thermotoga maritima*

<400> 37

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accctgggtgc cacgcggttc catggccgag ttcttcccgg agatcccga gatccagttc 120
gagggcaagg agtccaccaa cccgctcgcc ttccgcttct acgacccga cgaggtgatc 180
gacggcaagc cgctcaagga ccacctcaag ttctccgtgg ccttctggca caccttcgtg 240
aacgagggcc gcgacccggt cggcgacccg accgccgagc gcccggtgga ccgcttctcc 300
gacccgatgg acaaggcctt cgcccgcgtg gacgcccctt tcgagttctg cgagaagctc 360
aacatcgagt acttctgctt ccacgaccgc gacatcgccc cgagggcaa gaccctccgc 420
gagaccaaca agatcctcga caaggtggtg gagcgcatca aggagcgcat gaaggactcc 480
aacgtgaagc tcctctgggg caccgccaac ctcttctccc acccgcgcta catgcacggc 540
gccgccacca cctgctccgc cgacgtgttc gcctacgccg ccgcccaggt gaagaaggcc 600
ctggagatca ccaaggagct gggcggcgag ggctacgtgt tctggggcgg ccgaggggc 660
tacgagaccc tcctcaacac cgacctcggc ctggagctgg agaacctcgc ccgcttcctc 720
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aagccgaagg agccgaccaa gcaccagtac gacttcgacg tggccaccgc ctacgccttc 840
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gccaaggacg gcgtgttcga caagttcatc gaggagaagt accgctcctt caaggagggc 1260
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gacaaggagg acatcgagct gccgtccggc aagcaggagt acctggagtc cctcctcaac 1380
tcctacatcg tgaagaccat cgccgagctg cgctccgaga aggacgagct gtga 1434

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<210> 38

<211> 477

<212> PRT

<213> *Thermotoga maritima*

<400> 38

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Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
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Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Met Ala Glu Phe Phe
          20          25          30
Pro Glu Ile Pro Lys Ile Gln Phe Glu Gly Lys Glu Ser Thr Asn Pro
          35          40          45
Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val Ile Asp Gly Lys Pro
          50          55          60
Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe Trp His Thr Phe Val
          65          70          75          80
Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr Ala Glu Arg Pro Trp
          85          90          95
Asn Arg Phe Ser Asp Pro Met Asp Lys Ala Phe Ala Arg Val Asp Ala
          100          105          110
Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu Tyr Phe Cys Phe His
          115          120          125
Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu Arg Glu Thr Asn Lys
          130          135          140
Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu Arg Met Lys Asp Ser
          145          150          155          160
Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu Phe Ser His Pro Arg
          165          170          175
Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
          180          185          190
Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile Thr Lys Glu Leu Gly
          195          200          205
Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
          210          215          220

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Leu Asn Thr Asp Leu Gly Leu Glu Leu Glu Asn Leu Ala Arg Phe Leu
 225 230 235 240
 Arg Met Ala Val Glu Tyr Ala Lys Lys Ile Gly Phe Thr Gly Gln Phe
 245 250 255
 Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys His Gln Tyr Asp Phe
 260 265 270
 Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Asn His Gly Leu Asp Glu
 275 280 285
 Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala Thr Leu Ala Gly His
 290 295 300
 Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile Leu Gly Lys Leu Gly
 305 310 315 320
 Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu Gly Trp Asp Thr Asp
 325 330 335
 Gln Phe Pro Thr Asn Ile Tyr Asp Thr Thr Leu Ala Met Tyr Glu Val
 340 345 350
 Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu Asn Phe Asp Ala Lys
 355 360 365
 Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu Phe Ile Gly His Ile
 370 375 380
 Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys Ile Ala Tyr Lys Leu
 385 390 395 400
 Ala Lys Asp Gly Val Phe Asp Lys Phe Ile Glu Glu Lys Tyr Arg Ser
 405 410 415
 Phe Lys Glu Gly Ile Gly Lys Glu Ile Val Glu Gly Lys Thr Asp Phe
 420 425 430
 Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu Asp Ile Glu Leu Pro
 435 440 445
 Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Leu Asn Ser Tyr Ile Val
 450 455 460
 Lys Thr Ile Ala Glu Leu Arg Ser Glu Lys Asp Glu Leu
 465 470 475

<210> 39

<211> 1434

<212> DNA

<213> Thermotoga neapolitana

<400> 39

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 gagggcaagg agtccaccaa cccgctcgcc ttcaagttct acgacccgga ggagatcatc 180
 gacggcaagc cgctcaagga ccacctcaag ttctccgtgg ccttctggca caccttcgtg 240
 aacgagggcc gcgacccggt cggcgacccg accgccgacc gcccggtgga ccgctacacc 300
 gacccgatgg acaaggcctt cgcccgcgtg gacgccctct tcgagttctg cgagaagctc 360
 aacatcgagt acttctgctt ccacgaccgc gacatcgccc cgaggggcaa gaccctccgc 420
 gagaccaaca agatcctcga caaggtgggt gagcgcacatc aggagcgcac gaaggactcc 480
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 gccgccacca cctgctccgc cgacgtgttc gcctacgccg ccgcccaggt gaagaaggcc 600
 ctggagatca ccaaggagct gggcggcgag ggctacgtgt tctggggcgg ccgaggggc 660
 tacgagaccc tcctcaacac cgacctcggc ttcgagctgg agaacctcgc ccgcttcctc 720
 cgcattggccg tggactacgc caagcgcacg ggcttcaccg gccagttcct catcgagccg 780
 aagccgaagg agccgaccaa gcaccagtac gacttcgacg tggccaccgc ctacgccttc 840
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 atcgccgcgc acatcggtga gggcaagggt gacttcgaga agctggagga gtacatcatc 1320
 gacaaggaga ccatcgagct gccgtccggc aagcaggagt acctggagtc cctcatcaac 1380

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1434

<210> 40

<211> 477

<212> PRT

<213> Thermotoga neapolitana

<400> 40

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 20 25 30
 Pro Glu Ile Pro Lys Val Gln Phe Glu Gly Lys Glu Ser Thr Asn Pro
 35 40 45
 Leu Ala Phe Lys Phe Tyr Asp Pro Glu Glu Ile Ile Asp Gly Lys Pro
 50 55 60
 Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe Trp His Thr Phe Val
 65 70 75 80
 Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr Ala Asp Arg Pro Trp
 85 90 95
 Asn Arg Tyr Thr Asp Pro Met Asp Lys Ala Phe Ala Arg Val Asp Ala
 100 105 110
 Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu Tyr Phe Cys Phe His
 115 120 125
 Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu Arg Glu Thr Asn Lys
 130 135 140
 Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu Arg Met Lys Asp Ser
 145 150 155 160
 Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu Phe Ser His Pro Arg
 165 170 175
 Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
 180 185 190
 Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile Thr Lys Glu Leu Gly
 195 200 205
 Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
 210 215 220
 Leu Asn Thr Asp Leu Gly Phe Glu Leu Glu Asn Leu Ala Arg Phe Leu
 225 230 235 240
 Arg Met Ala Val Asp Tyr Ala Lys Arg Ile Gly Phe Thr Gly Gln Phe
 245 250 255
 Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys His Gln Tyr Asp Phe
 260 265 270
 Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Ser His Gly Leu Asp Glu
 275 280 285
 Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala Thr Leu Ala Gly His
 290 295 300
 Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile Leu Gly Lys Leu Gly
 305 310 315 320
 Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu Gly Trp Asp Thr Asp
 325 330 335
 Gln Phe Pro Thr Asn Val Tyr Asp Thr Thr Leu Ala Met Tyr Glu Val
 340 345 350
 Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu Asn Phe Asp Ala Lys
 355 360 365
 Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu Phe Ile Gly His Ile
 370 375 380
 Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys Val Ala Tyr Lys Leu
 385 390 395 400
 Val Lys Asp Gly Val Leu Asp Lys Phe Ile Glu Glu Lys Tyr Arg Ser
 405 410 415
 Phe Arg Glu Gly Ile Gly Arg Asp Ile Val Glu Gly Lys Val Asp Phe
 420 425 430
 Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu Thr Ile Glu Leu Pro

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435 440 445
 Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Ile Asn Ser Tyr Ile Val
 450 455 460
 Lys Thr Ile Leu Glu Leu Arg Ser Glu Lys Asp Glu Leu
 465 470 475

<210> 41
 <211> 1435
 <212> DNA
 <213> Thermotoga maritima

<400> 41
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 gagatcccga agatccagtt cgagggcaag gagtccacca acccgctcgc cttccgcttc 180
 tacgacccga acgaggtgat cgacggcaag ccgctcaagg accacctcaa gttctccgtg 240
 gccttcttggc acaccttcgt gaacgagggc cgcgacccgt tcggcgaccc gaccgccgag 300
 cgcccgtgga accgcttctc cgacccgatg gacaaggcct tcgcccgcgt ggacgccctc 360
 ttcgagttct gcgagaagct caacatcgag tactttctgct tccacgaccg cgacatcccc 420
 cggagggcaa gaccctccgc gagaccaaca agatcctcga caagggtggtg gagcgcatca 480
 aggagcgcat gaaggactcc aacgtgaagc tcctctggtgg caccgccaac ctcttctccc 540
 acccgcgcta catgcacggc gccgccacca cctgctccgc cgacgtgttc gcctacgccg 600
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 gccagttcct catcgagccg aagccgaagg agccgaccaa gcaccagtac gcttcgacgt 840
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 cgaggccaac caccgccacc tcgcccggcca cacttccag caccgagctgc gcatggcccc 960
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 ggccggcggc ttaccaagg gcggcctcaa cttcgacgcc aaggtgcgcc gcgcctccta 1140
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 caagatcgcc tacaagctcg ccaaggacgg cgtgttcgac aagttcatcg aggagaagta 1260
 ccgctccttc aaggagggca tcggcaagga gatcgtggag ggcaagaccg acttcgagaa 1320
 gctggaggag tacatcatcg acaaggagga catcgagctg ccgtccggca agcaggagta 1380
 cctggagtcc ctctcaact cctacatcgt gaagaccatc gccgagctgc gctga 1435

<210> 42
 <211> 478
 <212> PRT
 <213> Thermotoga maritima

<400> 42
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 Ile Pro Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Ile Gln Phe Glu
 35 40 45
 Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro Asn
 50 55 60
 Glu Val Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val
 65 70 75 80
 Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp
 85 90 95
 Pro Thr Ala Glu Arg Pro Trp Asn Arg Phe Ser Asp Pro Met Asp Lys
 100 105 110
 Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn
 115 120 125
 Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys
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 Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile

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	Ser	Ala	Asp	Val	Phe	Ala	Tyr	Ala	Ala	Ala	Gln	Val	Lys	Lys	Ala	Leu
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	Glu	Ile	Thr	Lys	Glu	Leu	Gly	Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly	Gly
		210					215					220				
	Arg	Glu	Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asp	Leu	Gly	Leu	Glu	Leu
225						230					235					240
	Glu	Asn	Leu	Ala	Arg	Phe	Leu	Arg	Met	Ala	Val	Glu	Tyr	Ala	Lys	Lys
				245						250					255	
	Ile	Gly	Phe	Thr	Gly	Gln	Phe	Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu	Pro
				260					265						270	
	Thr	Lys	His	Gln	Tyr	Asp	Phe	Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe	Leu
			275					280					285			
	Lys	Asn	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala	Asn
		290					295					300				
	His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met	Ala
305						310					315					320
	Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp	Leu
				325						330					335	
	Leu	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Ile	Tyr	Asp	Thr
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	Thr	Leu	Ala	Met	Tyr	Glu	Val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys	Gly
			355					360					365			
	Gly	Leu	Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val	Glu
		370					375					380				
	Asp	Leu	Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu	Gly
385						390					395					400
	Phe	Lys	Ile	Ala	Tyr	Lys	Leu	Ala	Lys	Asp	Gly	Val	Phe	Asp	Lys	Phe
				405						410					415	
	Ile	Glu	Glu	Lys	Tyr	Arg	Ser	Phe	Lys	Glu	Gly	Ile	Gly	Lys	Glu	Ile
			420						425					430		
	Val	Glu	Gly	Lys	Thr	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile	Asp
		435						440				445				
	Lys	Glu	Asp	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu	Ser
		450					455					460				
	Leu	Leu	Asn	Ser	Tyr	Ile	Val	Lys	Thr	Ile	Ala	Glu	Leu	Arg		
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<210> 43

<211> 1436

<212> DNA

<213> Thermotoga neapolitana

<400> 43

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tacgacccgg	aggagatcat	cgacggcaag	ccgctcaagg	accacctcaa	gttctccgtg	240
gccttctggc	acaccttcgt	gaacgagggc	cgcgacccgt	tcggcgaccc	gaccgccgac	300
cgcccgtgga	accgctacac	cgacccgatg	gacaaggcct	tcgcccgcgt	ggacgccctc	360
ttcgagttct	gcgagaagct	caacatcgag	tacttctgct	tccacgaccg	cgacatcccc	420
cggagggcaa	gaccctccgc	gagaccaaca	agatcctcga	caagggtggtg	gagcgcacatca	480
aggagcgcac	gaaggactcc	aacgtgaagc	tcctctgggg	caccgccaac	ctcttctccc	540
acccgcgcta	catgcacggc	gccgccacca	cctgctccgc	cgacgtgttc	gcctacgccg	600
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tctggggcgg	ccgcgagggc	tacgagaccc	tcctcaacac	cgacctcggc	ttcgagctgg	720
agaacctcgc	ccgcttcctc	cgcatggccg	tggtactacgc	caagcgcac	ggcttcaccg	780
gccagttcct	catcgagccg	aagccgaagg	agccgaccaa	gcaccagtac	gacttcgacg	840

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gcatcctcgg caagctcggc tccatcgacg ccaaccaggg cgacctcctc ctcggctggg 1020
acaccgacca gttcccgcacc aacgtgtacg acaccaccct cgccatgtac gaggtgatca 1080
aggccggcgg cttcaccaag ggcggcctca acttcgacgc caaggtgcgc cgcgcctcct 1140
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agctggagga gtacatcatc gacaaggaga ccatcgagct gccgtccggc aagcaggagt 1380
acctggagtc cctcatcaac tcctacatcg tgaagaccat cctggagctg cgctga 1436

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<210> 44

<211> 478

<212> PRT

<213> Thermotoga neapolitana

<400> 44

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35     40     45
Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro Glu
50     55     60
Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val
65     70     75     80
Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp
85     90     95
Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp Lys
100    105    110
Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn
115    120    125
Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys
130    135    140
Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile
145    150    155    160
Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala
165    170    175
Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys
180    185    190
Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu
195    200    205
Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly
210    215    220
Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu Leu
225    230    235    240
Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys Arg
245    250    255
Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro
260    265    270
Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu
275    280    285
Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn
290    295    300
His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala
305    310    315    320
Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu
325    330    335
Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp Thr
340    345    350
Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly
355    360    365

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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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 Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly
 385 390 395 400
 Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys Phe
 405 410 415
 Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp Ile
 420 425 430
 Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp
 435 440 445
 Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser
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 Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg
 465 470 475

<210> 45

<211> 1095

<212> PRT

<213> Aspergillus shirousami

<400> 45

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 35 40 45
 Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
 50 55 60
 Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
 65 70 75 80
 Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
 85 90 95
 Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
 100 105 110
 Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
 115 120 125
 Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
 130 135 140
 Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
 145 150 155 160
 Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
 165 170 175
 Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
 180 185 190
 Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
 195 200 205
 Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
 210 215 220
 Val Tyr Cys Ile Gly Glu Val Leu Asp Val Asp Pro Ala Tyr Thr Cys
 225 230 235 240
 Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
 245 250 255
 Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
 260 265 270
 Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
 275 280 285
 Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
 290 295 300
 Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
 305 310 315 320
 Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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Pro	Thr	Asp	Ser	Glu	Leu	Tyr	Lys	Leu	Ile	Ala	Ser	Ala	Asn	Ala	Ile		
		355					360					365					
Arg	Asn	Tyr	Ala	Ile	Ser	Lys	Asp	Thr	Gly	Phe	Val	Thr	Tyr	Lys	Asn		
	370					375					380						
Trp	Pro	Ile	Tyr	Lys	Asp	Asp	Thr	Thr	Ile	Ala	Met	Arg	Lys	Gly	Thr		
385					390					395					400		
Asp	Gly	Ser	Gln	Ile	Val	Thr	Ile	Leu	Ser	Asn	Lys	Gly	Ala	Ser	Gly		
			405					410						415			
Asp	Ser	Tyr	Thr	Leu	Ser	Leu	Ser	Gly	Ala	Gly	Tyr	Thr	Ala	Gly	Gln		
			420					425					430				
Gln	Leu	Thr	Glu	Val	Ile	Gly	Cys	Thr	Thr	Val	Thr	Val	Gly	Ser	Asp		
	435						440					445					
Gly	Asn	Val	Pro	Val	Pro	Met	Ala	Gly	Gly	Leu	Pro	Arg	Val	Leu	Tyr		
	450					455					460						
Pro	Thr	Glu	Lys	Leu	Ala	Gly	Ser	Lys	Ile	Cys	Ser	Ser	Ser	Lys	Pro		
465					470					475					480		
Ala	Thr	Leu	Asp	Ser	Trp	Leu	Ser	Asn	Glu	Ala	Thr	Val	Ala	Arg	Thr		
			485					490						495			
Ala	Ile	Leu	Asn	Asn	Ile	Gly	Ala	Asp	Gly	Ala	Trp	Val	Ser	Gly	Ala		
			500					505					510				
Asp	Ser	Gly	Ile	Val	Val	Ala	Ser	Pro	Ser	Thr	Asp	Asn	Pro	Asp	Tyr		
	515						520					525					
Phe	Tyr	Thr	Trp	Thr	Arg	Asp	Ser	Gly	Ile	Val	Leu	Lys	Thr	Leu	Val		
	530					535					540						
Asp	Leu	Phe	Arg	Asn	Gly	Asp	Thr	Asp	Leu	Leu	Ser	Thr	Ile	Glu	His		
545					550					555				560			
Tyr	Ile	Ser	Ser	Gln	Ala	Ile	Ile	Gln	Gly	Val	Ser	Asn	Pro	Ser	Gly		
			565					570						575			
Asp	Leu	Ser	Ser	Gly	Gly	Leu	Gly	Glu	Pro	Lys	Phe	Asn	Val	Asp	Glu		
			580					585					590				
Thr	Ala	Tyr	Ala	Gly	Ser	Trp	Gly	Arg	Pro	Gln	Arg	Asp	Gly	Pro	Ala		
	595						600					605					
Leu	Arg	Ala	Thr	Ala	Met	Ile	Gly	Phe	Gly	Gln	Trp	Leu	Leu	Asp	Asn		
	610				615						620						
Gly	Tyr	Thr	Ser	Ala	Ala	Thr	Glu	Ile	Val	Trp	Pro	Leu	Val	Arg	Asn		
625					630					635				640			
Asp	Leu	Ser	Tyr	Val	Ala	Gln	Tyr	Trp	Asn	Gln	Thr	Gly	Tyr	Asp	Leu		
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			805						810					815			
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Phe	Asp	Lys	Ser	Asp	Gly	Asp	Glu	Leu	Ser	Ala	Arg	Asp	Leu	Thr	Trp
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945					950					955					960
Thr	Gly	Ser	Gly	Gly	Val	Thr	Ser	Thr	Ser	Lys	Thr	Thr	Thr	Thr	Ala
			965						970					975	
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<211> 3285

<212> DNA

<213> Aspergillus shirousami

<400> 46

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<211> 679

<212> PRT

<213> Thermoanaerobacterium thermosaccharolyticum

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Pro Thr Ile Asp Thr Ala Asp Val Lys Glu Ile Lys Phe Ile Val Thr
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Lys Arg Asn Ser Leu Ile Met Lys Ala Lys Phe Glu Ala Leu Glu Gly
130     135     140
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Leu	Lys	Ala	Ser	Glu	Asp	Lys	Thr	Asn	Lys	Gly	Ala	Tyr	Ile	Ala	Ser	
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Tyr	Glu	Ile	Ala	Ala	Gly	Lys	Asp	Ala	Thr	Pro	Tyr	Val	Lys	Ala	Met	
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Glu	Lys	Phe	Ala	Asn	Glu	Gly	Gly	Ile	Ile	Ser	Glu	Gln	Val	Trp	Glu	
625				630						635					640	
Asp	Thr	Gly	Leu	Pro	Thr	Asp	Ser	Ala	Ser	Pro	Leu	Asn	Trp	Ala	His	
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Ala	Glu	Tyr	Val	Ile	Leu	Phe	Ala	Ser	Asn	Ile	Glu	His	Lys	Val	Leu	
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 <212> DNA
 <213> Thermoanaerobacterium thermosaccharolyticum

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 Asn Asn Gly Asn Thr Ile Ala Ala Ser Tyr Ser Ala Pro Ile Ser Gly
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 Ser Asn Tyr Glu Tyr Trp Thr Phe Ser Ala Ser Ile Asn Gly Ile Lys
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Lys	Gly	Leu	Asp	Val	Ser	Thr	Leu	Leu	Ala	Ala	Asn	Leu	Gly	Ser	Val	
385					390				395						400	
Asp	Asp	Gly	Phe	Phe	Thr	Pro	Gly	Ser	Glu	Lys	Ile	Leu	Ala	Thr	Ala	
			405						410					415		
Val	Ala	Val	Glu	Asp	Ser	Phe	Ala	Ser	Leu	Tyr	Pro	Ile	Asn	Lys	Asn	
			420					425					430			
Leu	Pro	Ser	Tyr	Leu	Gly	Asn	Ser	Ile	Gly	Arg	Tyr	Pro	Glu	Asp	Thr	
		435					440					445				
Tyr	Asn	Gly	Asn	Gly	Asn	Ser	Gln	Gly	Asn	Ser	Trp	Phe	Leu	Ala	Val	
	450				455						460					
Thr	Gly	Tyr	Ala	Glu	Leu	Tyr	Tyr	Arg	Ala	Ile	Lys	Glu	Trp	Ile	Gly	
465				470						475					480	
Asn	Gly	Gly	Val	Thr	Val	Ser	Ser	Ile	Ser	Leu	Pro	Phe	Phe	Lys	Lys	
			485						490					495		
Phe	Asp	Ser	Ser	Ala	Thr	Ser	Gly	Lys	Lys	Tyr	Thr	Val	Gly	Thr	Ser	
			500				505					510				
Asp	Phe	Asn	Asn	Leu	Ala	Gln	Asn	Ile	Ala	Leu	Ala	Ala	Asp	Arg	Phe	
		515					520				525					
Leu	Ser	Thr	Val	Gln	Leu	His	Ala	His	Asn	Asn	Gly	Ser	Leu	Ala	Glu	
	530					535					540					
Glu	Phe	Asp	Arg	Thr	Thr	Gly	Leu	Ser	Thr	Gly	Ala	Arg	Asp	Leu	Thr	
545				550						555					560	
Trp	Ser	His	Ala	Ser	Leu	Ile	Thr	Ala	Ser	Tyr	Ala	Lys	Ala	Gly	Ala	
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Pro	Ala	Ala														

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<210> 50
 <211> 1737
 <212> DNA
 <213> Rhizopus oryzae

<400> 50
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 ttctccggca aaatctacgt gaagaacatc gcctactcca agaagggtgac cgtgatctac 120
 gccgacggct ccgacaactg gaacaacaac ggcaacacca tcgccgcctc ctactccgcc 180
 ccgatctccg gctccaacta cgagtactgg accttctccg cctccatcaa cggcatcaag 240
 gagttctaca tcaagtacga ggtgtccggc aagacctact acgacaacaa caactccgcc 300
 aactaccagg tgtccacctc caagccgacc accaccaccg ccaccgccac caccaccacc 360
 gccccgtcca cctccaccac caccgccg tcccgtccg agccggccac cttcccgacc 420
 ggcaactcca ccatctctc ctggatcaag aagcaggagg gcatctcccg cttcgccatg 480
 ctccgcaaca tcaaccgcg gggctccgcc accggcttca tcgccgcctc cctctccacc 540
 gccggccccg actactacta cgcctggacc cgcgacgccg ccctcacctc caacgtgatc 600
 gtgtacgagt acaacaccac cctctccggc aacaagacca tcctcaacgt gctcaaggac 660
 tacgtgacct tctccgtgaa gaccagtc accctccaccg tgtgcaactg cctcggcgag 720
 ccgaagtcca acccggacgc ctccggctac accggcgctt ggggccgccc gcagaacgac 780
 ggcccggccg agcgcgccac caccttcac ctcttcgccg actcctacct caccagacc 840
 aaggacgcct cctacgtgac cggcaccctc aagccggcca tcttcaagga cctcgactac 900
 gtggtgaacg tgtggtccaa cggctgcttc gacctctggg aggaggtgaa cggcgtgcac 960
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 aacggcgact ccacccgcgc ctccacctac tcctccaccg cctccaccat cgccaacaaa 1080
 atctcctcct tctgggtgtc ctccaacaac tggatacagg tgtcccagtc cgtgaccggc 1140
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 gacgacggct tcttcacccc gggctccgag aagatcctcg ccaccgccgt ggccgtggag 1260
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 aacggcgggc tgaccgtgtc ctccatctcc ctcccgttct tcaagaagtt cgactcctcc 1500
 gccacctccg gcaagaagta caccgtgggc acctccgact tcaacaacct cgcccagAAC 1560
 atcgccctcg ccgccgaccg ctctctctcc accgtgcagc tccacgcccA caacaacggc 1620
 tccctcgcg aggagttcga ccgcaccacc ggctctcca ccggcgcccc cgacctcacc 1680
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<210> 51
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 51
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 20 25 30
 Gln Gly Phe Asn Trp Glu Ser Trp Lys Lys Gln Gly Gly Trp Tyr Asn
 35 40 45
 Tyr Leu Leu Gly Arg Val Asp Asp Ile Ala Ala Thr Gly Ala Thr His
 50 55 60
 Val Trp Leu Pro Gln Pro Ser His Ser Val Ala Pro Gln Gly Tyr Met
 65 70 75 80
 Pro Gly Arg Leu Tyr Asp Leu Asp Ala Ser Lys Tyr Gly Thr His Ala
 85 90 95
 Glu Leu Lys Ser Leu Thr Ala Ala Phe His Ala Lys Gly Val Gln Cys
 100 105 110
 Val Ala Asp Val Val Ile Asn His Arg Cys Ala Asp Tyr Lys Asp Gly
 115 120 125

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Arg	Gly	Ile	Tyr	Cys	Val	Phe	Glu	Gly	Gly	Thr	Pro	Asp	Ser	Arg	Leu
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Asp	Trp	Gly	Pro	Asp	Met	Ile	Cys	Ser	Asp	Asp	Thr	Gln	Tyr	Ser	Asn
145					150					155					160
Gly	Arg	Gly	His	Arg	Asp	Thr	Gly	Ala	Asp	Phe	Ala	Ala	Ala	Pro	Asp
				165					170					175	
Ile	Asp	His	Leu	Asn	Pro	Arg	Val	Gln	Gln	Glu	Leu	Ser	Asp	Trp	Leu
			180					185					190		
Asn	Trp	Leu	Lys	Ser	Asp	Leu	Gly	Phe	Asp	Gly	Trp	Arg	Leu	Asp	Phe
		195					200					205			
Ala	Lys	Gly	Tyr	Ser	Ala	Ala	Val	Ala	Lys	Val	Tyr	Val	Asp	Ser	Thr
	210					215					220				
Ala	Pro	Thr	Phe	Val	Val	Ala	Glu	Ile	Trp	Ser	Ser	Leu	His	Tyr	Asp
225					230					235					240
Gly	Asn	Gly	Glu	Pro	Ser	Ser	Asn	Gln	Asp	Ala	Asp	Arg	Gln	Glu	Leu
				245					250					255	
Val	Asn	Trp	Ala	Gln	Ala	Val	Gly	Gly	Pro	Ala	Ala	Ala	Phe	Asp	Phe
			260					265					270		
Thr	Thr	Lys	Gly	Val	Leu	Gln	Ala	Val	Gln	Gly	Glu	Leu	Trp	Arg	
		275				280					285				
Met	Lys	Asp	Gly	Asn	Gly	Lys	Ala	Pro	Gly	Met	Ile	Gly	Trp	Leu	Pro
	290					295					300				
Glu	Lys	Ala	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Thr	Gly	Ser	Thr	Gln
305					310					315					320
Asn	Ser	Trp	Pro	Phe	Pro	Ser	Asp	Lys	Val	Met	Gln	Gly	Tyr	Ala	Tyr
				325					330					335	
Ile	Leu	Thr	His	Pro	Gly	Thr	Pro	Cys	Ile	Phe	Tyr	Asp	His	Val	Phe
			340					345					350		
Asp	Trp	Asn	Leu	Lys	Gln	Glu	Ile	Ser	Ala	Leu	Ser	Ala	Val	Arg	Ser
		355					360					365			
Arg	Asn	Gly	Ile	His	Pro	Gly	Ser	Glu	Leu	Asn	Ile	Leu	Ala	Ala	Asp
	370					375					380				
Gly	Asp	Leu	Tyr	Val	Ala	Lys	Ile	Asp	Asp	Lys	Val	Ile	Val	Lys	Ile
385					390					395					400
Gly	Ser	Arg	Tyr	Asp	Val	Gly	Asn	Leu	Ile	Pro	Ser	Asp	Phe	His	Ala
				405					410					415	
Val	Ala	His	Gly	Asn	Asn	Tyr	Cys	Val	Trp	Glu	Lys	His	Gly	Leu	Arg
			420					425					430		
Val	Pro	Ala	Gly	Arg	His	His									
			435												

<210> 52
 <211> 1320
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 52
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 aagaagcaag gtgggtggtg caactacctc ctggggcggg tggacgacat cgccgcgacg 180
 ggggccacgc acgtctggct cccgcagccg tcgcactcgg tggcgccgca ggggtacatg 240
 cccggccggc tctacgacct ggacgcgtcc aagtacggca cccacgcgga gctcaagtcg 300
 ctcaccgcgg cgttccacgc caagggcgtc cagtgcgtcg ccgacgtcgt gatcaaccac 360
 cgctgcgccg actacaagga cggccgcggc atctactgcg tcttcgaggg cggcacgccc 420
 gacagccgcc tcgactgggg ccccacatg atctgcagcg acgacacgca gtactccaac 480
 gggcgcgggc accgcgacac gggggccgac ttcgccgccg cgcccgacat cgaccacctc 540
 aaccgcgcgc tgcagcagga gctctcggac tggctcaact ggctcaagtc cgacctcggc 600
 ttcgacggct ggcgcctcga cttcgccaag ggctactccg ccgccgtcgc caaggtgtac 660
 gtcgacagca ccgccccac cttcgtcgtc gccgagatat ggagctccct ccactacgac 720

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gccgtccagg gcgagctgtg gcgcatgaag gacggcaacg gcaagggcgc cgggatgac 900
ggctggctgc cggagaaggc cgtcacgttc gtcgacaacc acgacaccgg ctccacgcag 960
aactcgtggc cattccccctc cgacaaggtc atgcagggct acgcctatat cctcacgcac 1020
ccaggaactc catgcatctt ctacgaccac gttttcgact ggaacctgaa gcaggagatc 1080
agcgcgctgt ctgcggtgag gtcaagaaac gggatccacc cggggagcga gctgaacatc 1140
ctcgccgccg acggggatct ctacgtcgcc aagattgacg acaaggatcat cgtgaagatc 1200
gggtcacggt acgacgtcgg gaacctgatc ccctcagact tccacgccgt tgcccctggc 1260
aacaactact gcgtttggga gaagcacggt ctgagagttc cagcggggcg gcaccactag 1320

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<210> 53
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 53
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 Val Thr Ser Thr Ser Lys Thr Thr Thr Thr Ala Ser Lys Thr Ser Thr
 20 25 30
 Thr Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val
 35 40 45

<210> 54
 <211> 137
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic

<400> 54
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 tccaagacca ccaccaccgc ctccaagacc tccaccacca cctcctccac ctctgcacc 120
 accccgaccg ccgtgtc 137

<210> 55
 <211> 300
 <212> PRT
 <213> Pyrococcus furiosus

<400> 55
 Ile Tyr Phe Val Glu Lys Tyr His Thr Ser Glu Asp Lys Ser Thr Ser
 1 5 10 15
 Asn Thr Ser Ser Thr Pro Pro Gln Thr Thr Leu Ser Thr Thr Lys Val
 20 25 30
 Leu Lys Ile Arg Tyr Pro Asp Asp Gly Glu Trp Pro Gly Ala Pro Ile
 35 40 45
 Asp Lys Asp Gly Asp Gly Asn Pro Glu Phe Tyr Ile Glu Ile Asn Leu
 50 55 60
 Trp Asn Ile Leu Asn Ala Thr Gly Phe Ala Glu Met Thr Tyr Asn Leu
 65 70 75 80
 Thr Ser Gly Val Leu His Tyr Val Gln Gln Leu Asp Asn Ile Val Leu
 85 90 95
 Arg Asp Arg Ser Asn Trp Val His Gly Tyr Pro Glu Ile Phe Tyr Gly
 100 105 110
 Asn Lys Pro Trp Asn Ala Asn Tyr Ala Thr Asp Gly Pro Ile Pro Leu
 115 120 125

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Pro Ser Lys Val Ser Asn Leu Thr Asp Phe Tyr Leu Thr Ile Ser Tyr
130 135 140
Lys Leu Glu Pro Lys Asn Gly Leu Pro Ile Asn Phe Ala Ile Glu Ser
145 150 155 160
Trp Leu Thr Arg Glu Ala Trp Arg Thr Thr Gly Ile Asn Ser Asp Glu
165 170 175
Gln Glu Val Met Ile Trp Ile Tyr Tyr Asp Gly Leu Gln Pro Ala Gly
180 185 190
Ser Lys Val Lys Glu Ile Val Val Pro Ile Ile Val Asn Gly Thr Pro
195 200 205
Val Asn Ala Thr Phe Glu Val Trp Lys Ala Asn Ile Gly Trp Glu Tyr
210 215 220
Val Ala Phe Arg Ile Lys Thr Pro Ile Lys Glu Gly Thr Val Thr Ile
225 230 235 240
Pro Tyr Gly Ala Phe Ile Ser Val Ala Ala Asn Ile Ser Ser Leu Pro
245 250 255
Asn Tyr Thr Glu Leu Tyr Leu Glu Asp Val Glu Ile Gly Thr Glu Phe
260 265 270
Gly Thr Pro Ser Thr Thr Ser Ala His Leu Glu Trp Trp Ile Thr Asn
275 280 285
Ile Thr Leu Thr Pro Leu Asp Arg Pro Leu Ile Ser
290 295 300

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<210> 56

<211> 903

<212> DNA

<213> Pyrococcus furiosus

<400> 56

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ggcgagtggc ccggcgcccc gatcgacaag gacggcgacg gcaaccgga gttctacatc 180
gagatcaacc tctggaacat cctcaacgcc accggcttcg ccgagatgac ctacaacctc 240
actagtggcg tgctccacta cgtgcagcag ctcgacaaca tcgtgctccg cgaccgctcc 300
aactgggtgc acggctaccc ggaaatcttc tacggcaaca agccgtggaa cgccaactac 360
gccaccgacg gcccgatccc gctcccgtcc aagggtgtcca acctcaccga cttctacctc 420
accatctcct acaagctcga gccgaagaac ggtctcccga tcaacttcgc catcgagtcc 480
tggtcaccac gcgaggcctg gcgcaccacc ggcatacaact ccgacgagca ggaggtgatg 540
atctggatct actacgacgg cctccagccc gcgggctcca aggtgaagga gatcgtggtg 600
ccgatcatcg tgaacggcac ccggtgaac gccaccttcg aggtgtggaa ggccaacatc 660
ggctgggagt acgtggcctt ccgcatcaag accccgatca aggagggcac cgtgaccatc 720
ccgtacggcg cttcatctc cgtggccgcc aacatctcct ccctcccga ctacaccgag 780
aagtacctcg aggacgtgga gatcggcacc gagttcggca ccccggtccac cacctccgcc 840
cacctcgagt ggtggatcac caacatcacc ctcaccccg ctcgaccgcc gctcatctcc 900
tag 903

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<210> 57

<211> 387

<212> PRT

<213> Thermus flavus

<400> 57

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20 25 30
Leu Asp Pro Val Tyr Val Val His Lys Leu Ala Glu Leu Gly Ala Tyr
35 40 45
Gly Val Asn Leu His Asp Glu Asp Leu Ile Pro Arg Gly Thr Pro Pro
50 55 60
Gln Glu Arg Asp Gln Ile Val Arg Arg Phe Lys Lys Ala Leu Asp Glu
65 70 75 80

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60110USPCT1 Corrected SEQ LIST 2-2007.txt

Thr Val Leu Lys Val Pro Met Val Thr Ala Asn Leu Phe Ser Glu Pro
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 Ala Phe Arg Asp Gly Ala Ser Thr Thr Arg Asp Pro Trp Val Trp Ala
 100 105 110
 Tyr Ala Leu Arg Lys Ser Leu Glu Thr Met Asp Leu Gly Ala Glu Leu
 115 120 125
 Gly Ala Glu Ile Tyr Met Phe Trp Met Val Arg Glu Arg Ser Glu Val
 130 135 140
 Glu Ser Thr Asp Lys Thr Arg Lys Val Trp Asp Trp Val Arg Glu Thr
 145 150 155 160
 Leu Asn Phe Met Thr Ala Tyr Thr Glu Asp Gln Gly Tyr Gly Tyr Arg
 165 170 175
 Phe Ser Val Glu Pro Lys Pro Asn Glu Pro Arg Gly Asp Ile Tyr Phe
 180 185 190
 Thr Thr Val Gly Ser Met Leu Ala Leu Ile His Thr Leu Asp Arg Pro
 195 200 205
 Glu Arg Phe Gly Leu Asn Pro Glu Phe Ala His Glu Thr Met Ala Gly
 210 215 220
 Leu Asn Phe Asp His Ala Val Ala Gln Ala Val Asp Ala Gly Lys Leu
 225 230 235 240
 Phe His Ile Asp Leu Asn Asp Gln Arg Met Ser Arg Phe Asp Gln Asp
 245 250 255
 Leu Arg Phe Gly Ser Glu Asn Leu Lys Ala Gly Phe Phe Leu Val Asp
 260 265 270
 Leu Leu Glu Ser Ser Gly Tyr Gln Gly Pro Arg His Phe Glu Ala His
 275 280 285
 Ala Leu Arg Thr Glu Asp Glu Glu Gly Val Trp Thr Phe Val Arg Val
 290 295 300
 Cys Met Arg Thr Tyr Leu Ile Ile Lys Val Arg Ala Glu Thr Phe Arg
 305 310 315 320
 Glu Asp Pro Glu Val Lys Glu Leu Leu Ala Ala Tyr Tyr Gln Glu Asp
 325 330 335
 Pro Ala Thr Leu Ala Leu Leu Asp Pro Tyr Ser Arg Glu Lys Ala Glu
 340 345 350
 Ala Leu Lys Arg Ala Glu Leu Pro Leu Glu Thr Lys Arg Arg Arg Gly
 355 360 365
 Tyr Ala Leu Glu Arg Leu Asp Gln Leu Ala Val Glu Tyr Leu Leu Gly
 370 375 380
 Val Arg Gly
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<210> 58

<211> 978

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 58

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 tccaacacct cctccacccc gccgcagacc accctctcca ccaccaaggt gctcaagatc 180
 cgctacccgg acgacggtga gtggcccggc gcccgatcg acaaggacgg cgacggcaac 240
 ccggagttct acatcgagat caacctctgg aacatcctca acgccaccgg cttcgccgag 300
 atgacctaca acctcactag tggcgtgctc cactacgtgc agcagctcga caacatcgtg 360
 ctccgcgacc gctccaactg ggtgcacggc taccggaata tcttctacgg caacaagccg 420
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 aaggagatcg tggtgccgat catcgtgaac ggcaccccgg tgaacgccac cttcgaggtg 720

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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ccgaactaca	ccgagaagta	cctcgaggac	gtggagatcg	gcaccgagtt	cggcaccctg	900
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cgcccgtctc	tctcctag					978

<210> 59
 <211> 1920
 <212> DNA
 <213> Aspergillus niger

<400> 59

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gccatcctca	acaacatcgg	cgccgacggc	gcctgggtgt	ccggcgccga	ctccggcatc	180
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tacaagttca	tccgcatcga	gtccgacgac	tccgtggagt	gggagtccga	cccgaaccgc	1860
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<210> 60
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 60
 Ser Glu Lys Asp Glu Leu
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<210> 61
 <211> 561
 <212> DNA

<213> Artificial Sequence

<220>

<223> Xylanase BD7436

<220>

<221> CDS

<222> (1)..(561)

<400> 61

atg	gct	agc	acc	ttc	tac	tgg	cat	ttg	tgg	acc	gac	ggc	atc	ggc	acc	48
Met	Ala	Ser	Thr	Phe	Tyr	Trp	His	Leu	Trp	Thr	Asp	Gly	Ile	Gly	Thr	
1				5				10					15			

gtg	aac	gct	acc	aac	ggc	agc	gac	ggc	aac	tac	agc	gtg	agc	tgg	agc	96
Val	Asn	Ala	Thr	Asn	Gly	Ser	Asp	Gly	Asn	Tyr	Ser	Val	Ser	Trp	Ser	
			20					25					30			

aac	tgc	ggc	aac	ttc	gtg	gtg	ggc	aag	ggc	tgg	acc	acc	ggc	agc	gct	144
Asn	Cys	Gly	Asn	Phe	Val	Val	Gly	Lys	Gly	Trp	Thr	Thr	Gly	Ser	Ala	
		35					40					45				

acc	agg	gtg	atc	aac	tac	aac	gct	cat	gct	ttc	agc	gtg	gtg	ggc	aac	192
Thr	Arg	Val	Ile	Asn	Tyr	Asn	Ala	His	Ala	Phe	Ser	Val	Val	Gly	Asn	
	50					55					60					

gct	tac	ttg	gct	ttg	tac	ggc	tgg	acc	agg	aac	agc	ttg	atc	gag	tac	240
Ala	Tyr	Leu	Ala	Leu	Tyr	Gly	Trp	Thr	Arg	Asn	Ser	Leu	Ile	Glu	Tyr	
65				70					75					80		

tac	gtg	gtg	gac	agc	tgg	ggc	acc	tac	agg	cca	acc	ggc	acc	tac	aag	288
Tyr	Val	Val	Asp	Ser	Trp	Gly	Thr	Tyr	Arg	Pro	Thr	Gly	Thr	Tyr	Lys	
			85					90						95		

ggc	acc	gtg	acc	agc	gac	ggc	ggc	acc	tac	gac	atc	tac	acc	acc	acc	336
Gly	Thr	Val	Thr	Ser	Asp	Gly	Gly	Thr	Tyr	Asp	Ile	Tyr	Thr	Thr	Thr	
			100					105					110			

agg	acc	aac	gct	cca	agc	atc	gac	ggc	aac	aac	acc	acc	ttc	acc	caa	384
Arg	Thr	Asn	Ala	Pro	Ser	Ile	Asp	Gly	Asn	Asn	Thr	Thr	Phe	Thr	Gln	
		115					120					125				

ttc	tgg	agc	gtg	agg	caa	agc	aag	agg	cca	atc	ggc	acc	aac	aac	acc	432
Phe	Trp	Ser	Val	Arg	Gln	Ser	Lys	Arg	Pro	Ile	Gly	Thr	Asn	Asn	Thr	
	130					135					140					

atc	acc	ttc	agc	aac	cat	gtg	aac	gct	tgg	aag	agc	aag	ggc	atg	aac	480
Ile	Thr	Phe	Ser	Asn	His	Val	Asn	Ala	Trp	Lys	Ser	Lys	Gly	Met	Asn	
145					150					155				160		

ttg	ggc	agc	agc	tgg	agc	tac	caa	gtg	ttg	gct	acc	gag	ggc	tac	caa	528
Leu	Gly	Ser	Ser	Trp	Ser	Tyr	Gln	Val	Leu	Ala	Thr	Glu	Gly	Tyr	Gln	
				165					170					175		

agc	agc	ggc	tac	agc	aac	gtg	acc	gtg	tgg	tag						561
Ser	Ser	Gly	Tyr	Ser	Asn	Val	Thr	Val	Trp							
			180					185								

<210> 62

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 62

Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr
1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn
50 55 60

Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 63

<211> 561

<212> DNA

<213> Artificial Sequence

<220>

<223> xylanase BD6002A

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>

<221> CDS

<222> (1)..(561)

<400> 63

atg gct agc acc gac tac tgg caa aac tgg acc gac ggc ggc ggc acc	48
Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr	
1 5 10 15	
gtg aac gct acc aac ggc agc gac ggc aac tac agc gtg agc tgg agc	96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser	
20 25 30	
aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc agc gct	144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala	
35 40 45	
acc agg gtg atc aac tac aac gct ggc gct ttc agc cca agc ggc aac	192
Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn	
50 55 60	
ggc tac ttg gct ttg tac ggc tgg acc agg aac agc ttg atc gag tac	240
Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr	
65 70 75 80	
tac gtg gtg gac agc tgg ggc acc tac agg cca acc ggc acc tac aag	288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys	
85 90 95	
ggc acc gtg acc agc gac ggc ggc acc tac gac atc tac acc acc acc	336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr	
100 105 110	
agg acc aac gct cca agc atc gac ggc aac aac acc acc ttc acc caa	384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln	
115 120 125	
ttc tgg agc gtg agg caa agc aag agg cca atc ggc acc aac aac acc	432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr	
130 135 140	
atc acc ttc agc aac cat gtg aac gct tgg aag agc aag ggc atg aac	480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn	
145 150 155 160	
ttg ggc agc agc tgg agc tac caa gtg ttg gct acc gag ggc tac caa	528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln	
165 170 175	
agc agc ggc tac agc aac gtg acc gtg tgg tag	561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp	
180 185	

<210> 64

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<400> 64

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 65

<211> 561

<212> DNA

<213> Artificial Sequence

<220>

<223> xylanase BD6002B

<220>

<221> CDS

<222> (1)..(561)

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<400> 65
 atg gcc tcc acc gac tac tgg cag aac tgg acc gac ggc ggc ggc acc 48
 Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
 1 5 10 15

gtg aac gcc acc aac ggc tcc gac ggc aac tac tcc gtg tcc tgg tcc 96
 Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30

aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc tcc gcc 144
 Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45

acc cgc gtg atc aac tac aac gcc ggc gcc ttc tcc ccg tcc ggc aac 192
 Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
 50 55 60

ggc tac ctc gcc ctc tac ggc tgg acc cgc aac tcc ctc atc gag tac 240
 Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80

tac gtg gtg gac tcc tgg ggc acc tac cgc ccg acc ggc acc tac aag 288
 Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95

ggc acc gtg acc tcc gac ggc ggc acc tac gac atc tac acc acc acc 336
 Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110

cgc acc aac gcc ccg tcc atc gac ggc aac aac acc acc ttc acc cag 384
 Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125

ttc tgg tcc gtg cgc cag tcc aag cgc ccg atc ggc acc aac aac acc 432
 Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140

atc acc ttc tcc aac cac gtg aac gcc tgg aag tcc aag ggc atg aac 480
 Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160

ctc ggc tcc tcc tgg tcc tac cag gtg ctc gcc acc gag ggc tac cag 528
 Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175

tcc tcc ggc tac tcc aac gtg acc gtg tgg tga 561
 Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

<210> 66
 <211> 186
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 66

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
 1 5 10 15

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 67
<211> 2071
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (1)..(2071)
<223> Promoter

<400> 67
tccatgctgt cctactactt gcttcatccc cttctacatt ttgttctggt ttttggcctg 60
catttcggat catgatgtat gtgatttcca atctgctgca atatgaatgg agactctgtg 120
ctaaccatca acaacatgaa atgcttatga ggcctttgct gagcagccaa tcttgcctgt 180

60110USPCT1 Corrected SEQ LIST 2-2007.txt

gtttatgtct tcacaggccg aattcctctg ttttgttttt caccctcaat atttggaac	240
atttatctag gttgtttggtg tccaggccta taaatcatac atgatgttgt cgtattggat	300
gtgaatgtgg tggcgtgttc agtgccttggt atttgagttt gatgagagtt gcttctgggt	360
caccactcac cattatcgat gctcctcttc agcataaggt aaaagtcttc cctgtttacg	420
ttattttacc cactatgggtt gcttggggttg gttttttcct gattgcttat gccatggaaa	480
gtcatttgat atgttgaact tgaattaact gtagaattgt atacatgttc catttggtgtt	540
gtacttcctt cttttctatt agtagcctca gatgagtgtg aaaaaaacag attatataac	600
ttgccctata aatcatttga aaaaaatatt gtacagtgtg aaattgatat atagtgaatt	660
tttaagagca tgttttccta aagaagtata tattttctat gtacaaaggc cattgaagta	720
attgtagata caggataatg tagacttttt ggacttacac tgctaccttt aagtaacaat	780
catgagcaat agtgttgcaa tgatathtag gctgcattcg ttactctct tgatttccat	840
gagcacgctt cccaaactgt taaactctgt gttttttgcc aaaaaaaat gcataggaaa	900
gttgctttta aaaaatcata tcaatccatt ttttaagtta tagctaatac ttaattaatc	960
atgcgctaata agtcactct gtttttcgta ctagagagat tgttttgaac cagcactcaa	1020
gaacacagcc ttaaccagc caaataatgc tacaacctac cagtccacac ctcttgtaaa	1080
gcatttggtg catggaaaag ctaagatgac agcaacctgt tcaggaaaac aactgacaag	1140
gtcataggga gaggagctt ttggaaagggt gccgtgcagt tcaaacaatt agttagcagt	1200
agggtgttg tttttgctca cagcaataag aagttaatca tgggtgtaggc aaccxaaata	1260
aaacaccaa atatgcacaa ggcagtttgt tgtattctgt agtacagaca aaactaaaag	1320
taatgaaaga agatgtgggtg ttagaaaagg aaacaatatc atgagtaatg tgtgggcatt	1380
atgggaccac gaaataaaaa gaacattttg atgagtcgtg tctctcgat gagcctcaaa	1440
agttctctca ccccgataa gaaaccctta agcaatgtgc aaagtttgca ttctccactg	1500
acataatgca aaataagata tcatcgatga catagcaact catgcatcat atcatgcctc	1560
tctcaacctt ttcattccta ctcatctaca taagtatctt cagctaaatg ttagaacata	1620
aaccataag tcacgtttga tgagtattag gcgtgacaca tgacaaatca cagactcaag	1680
caagataaag caaatgatg tgtacataaa actccagagc tatatgtcat attgcaaaaa	1740
gaggagagct tataagacaa ggcattgactc acaaaaattc atttgccttt cgtgtcaaaa	1800
agaggagggc ttacattat ccatgtcata ttgcaaaaga aagagagaaa gaacaacaca	1860
atgctgcgtc aattatacat atctgtatgt ccatcattat tcatccacct ttcgtgtacc	1920
acacttcata tatcatgagt cacttcatgt ctggacatta acaaaactcta tcttaacatt	1980
tagatgcaag agcctttatc tcactataaa tgcacgatga tttctcattg tttctcacia	2040
aaagcattca gttcattagt cctacaacaa c	2071

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<210> 68
 <211> 79
 <212> PRT
 <213> Zea mays

<220>
 <221> SIGNAL
 <222> (1)..(79)
 <223> Maize waxy signal sequence.

<400> 68

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
 1 5 10 15

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
 20 25 30

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
 35 40 45

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
 50 55 60

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala
 65 70 75

<210> 69
 <211> 1005
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Bromelain Sequence

<220>
 <221> CDS
 <222> (1)..(1005)
 <223> Synthetic Bromelain

<400> 69

atg gcc tgg aag gtg cag gtg gtg ttc ctc ttc ctc ttc ctc tgc gtg 48
 Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
 1 5 10 15

atg tgg gcc tcc ccg tcc gcc gcc tcc gcg gac gag ccg tcc gac ccg 96
 Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
 20 25 30

atg atg aag cgc ttc gag gag tgg atg gtg gag tac ggc cgc gtg tac 144
 Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
 35 40 45

aag gac aac gac gag aag atg cgc cgc ttc cag atc ttc aag aac aac 192

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Lys	Asp	Asn	Asp	Glu	Lys	Met	Arg	Arg	Phe	Gln	Ile	Phe	Lys	Asn	Asn	
50					55					60						
gtg	aac	cac	atc	gag	acc	ttc	aac	tcc	cgc	aac	gag	aac	tcc	tac	acc	240
Val	Asn	His	Ile	Glu	Thr	Phe	Asn	Ser	Arg	Asn	Glu	Asn	Ser	Tyr	Thr	
65					70					75					80	
ctc	ggc	atc	aac	cag	ttc	acc	gac	atg	acc	aac	aac	gag	ttc	atc	gcc	288
Leu	Gly	Ile	Asn	Gln	Phe	Thr	Asp	Met	Thr	Asn	Asn	Glu	Phe	Ile	Ala	
				85					90					95		
cag	tac	acc	ggc	ggc	atc	tcc	cgc	ccg	ctc	aac	atc	gag	cgc	gag	ccg	336
Gln	Tyr	Thr	Gly	Gly	Ile	Ser	Arg	Pro	Leu	Asn	Ile	Glu	Arg	Glu	Pro	
			100					105					110			
gtg	gtg	tcc	ttc	gac	gac	gtg	gac	atc	tcc	gcc	gtg	ccg	cag	tcc	atc	384
Val	Val	Ser	Phe	Asp	Asp	Val	Asp	Ile	Ser	Ala	Val	Pro	Gln	Ser	Ile	
		115				120						125				
gac	tgg	cgc	gac	tac	ggc	gcc	gtg	acc	tcc	gtg	aag	aac	cag	aac	ccg	432
Asp	Trp	Arg	Asp	Tyr	Gly	Ala	Val	Thr	Ser	Val	Lys	Asn	Gln	Asn	Pro	
	130					135					140					
tgc	ggc	gcc	tgc	tgg	gcc	ttc	gcc	gcc	atc	gcc	acc	gtg	gag	tcc	atc	480
Cys	Gly	Ala	Cys	Trp	Ala	Phe	Ala	Ala	Ile	Ala	Thr	Val	Glu	Ser	Ile	
145					150					155					160	
tac	aag	atc	aag	aag	ggc	atc	ctc	gag	ccg	ctc	tcc	gag	cag	cag	gtg	528
Tyr	Lys	Ile	Lys	Lys	Gly	Ile	Leu	Glu	Pro	Leu	Ser	Glu	Gln	Gln	Val	
				165					170					175		
ctc	gac	tgc	gcc	aag	ggc	tac	ggc	tgc	aag	ggc	ggc	tgg	gag	ttc	cgc	576
Leu	Asp	Cys	Ala	Lys	Gly	Tyr	Gly	Cys	Lys	Gly	Gly	Trp	Glu	Phe	Arg	
			180					185					190			
gcc	ttc	gag	ttc	atc	atc	tcc	aac	aag	ggc	gtg	gcc	tcc	ggc	gcc	atc	624
Ala	Phe	Glu	Phe	Ile	Ile	Ser	Asn	Lys	Gly	Val	Ala	Ser	Gly	Ala	Ile	
		195				200						205				
tac	ccg	tac	aag	gcc	gcc	aag	ggc	acc	tgc	aag	acc	gac	ggc	gtg	ccg	672
Tyr	Pro	Tyr	Lys	Ala	Ala	Lys	Gly	Thr	Cys	Lys	Thr	Asp	Gly	Val	Pro	
	210					215					220					
aac	tcc	gcc	tac	atc	acc	ggc	tac	gcc	cgc	gtg	ccg	cgc	aac	aac	gag	720
Asn	Ser	Ala	Tyr	Ile	Thr	Gly	Tyr	Ala	Arg	Val	Pro	Arg	Asn	Asn	Glu	
225					230					235					240	
tcc	tcc	atg	atg	tac	gcc	gtg	tcc	aag	cag	ccg	atc	acc	gtg	gcc	gtg	768
Ser	Ser	Met	Met	Tyr	Ala	Val	Ser	Lys	Gln	Pro	Ile	Thr	Val	Ala	Val	
				245					250					255		
gac	gcc	aac	gcc	aac	ttc	cag	tac	tac	aag	tcc	ggc	gtg	ttc	aac	ggc	816
Asp	Ala	Asn	Ala	Asn	Phe	Gln	Tyr	Tyr	Lys	Ser	Gly	Val	Phe	Asn	Gly	
			260				265						270			
ccg	tgc	ggc	acc	tcc	ctc	aac	cac	gcc	gtg	acc	gcc	atc	ggc	tac	ggc	864
Pro	Cys	Gly	Thr	Ser	Leu	Asn	His	Ala	Val	Thr	Ala	Ile	Gly	Tyr	Gly	
		275					280					285				
cag	gac	tcc	atc	atc	tac	ccg	aag	aag	tgg	ggc	gcc	aag	tgg	ggc	gag	912
Gln	Asp	Ser	Ile	Ile	Tyr	Pro	Lys	Lys	Trp	Gly	Ala	Lys	Trp	Gly	Glu	
	290					295					300					

60110USPCT1 Corrected SEQ LIST 2-2007.txt

gcc ggc tac atc cgc atg gcc cgc gac gtg tcc tcc tcc tcc ggc atc 960
Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
305 310 315 320

tgc ggc atc gcc atc gac ccg ctc tac ccg acc ctc gag gag tag 1005
Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
325 330

<210> 70
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 70

Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
20 25 30

Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
35 40 45

Lys Asp Asn Asp Glu Lys Met Arg Arg Phe Gln Ile Phe Lys Asn Asn
50 55 60

Val Asn His Ile Glu Thr Phe Asn Ser Arg Asn Glu Asn Ser Tyr Thr
65 70 75 80

Leu Gly Ile Asn Gln Phe Thr Asp Met Thr Asn Asn Glu Phe Ile Ala
85 90 95

Gln Tyr Thr Gly Gly Ile Ser Arg Pro Leu Asn Ile Glu Arg Glu Pro
100 105 110

Val Val Ser Phe Asp Asp Val Asp Ile Ser Ala Val Pro Gln Ser Ile
115 120 125

Asp Trp Arg Asp Tyr Gly Ala Val Thr Ser Val Lys Asn Gln Asn Pro
130 135 140

Cys Gly Ala Cys Trp Ala Phe Ala Ala Ile Ala Thr Val Glu Ser Ile
145 150 155 160

Tyr Lys Ile Lys Lys Gly Ile Leu Glu Pro Leu Ser Glu Gln Gln Val
165 170 175

Leu Asp Cys Ala Lys Gly Tyr Gly Cys Lys Gly Gly Trp Glu Phe Arg
 180 185 190

Ala Phe Glu Phe Ile Ile Ser Asn Lys Gly Val Ala Ser Gly Ala Ile
 195 200 205

Tyr Pro Tyr Lys Ala Ala Lys Gly Thr Cys Lys Thr Asp Gly Val Pro
 210 215 220

Asn Ser Ala Tyr Ile Thr Gly Tyr Ala Arg Val Pro Arg Asn Asn Glu
 225 230 235 240

Ser Ser Met Met Tyr Ala Val Ser Lys Gln Pro Ile Thr Val Ala Val
 245 250 255

Asp Ala Asn Ala Asn Phe Gln Tyr Tyr Lys Ser Gly Val Phe Asn Gly
 260 265 270

Pro Cys Gly Thr Ser Leu Asn His Ala Val Thr Ala Ile Gly Tyr Gly
 275 280 285

Gln Asp Ser Ile Ile Tyr Pro Lys Lys Trp Gly Ala Lys Trp Gly Glu
 290 295 300

Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
 305 310 315 320

Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
 325 330

<210> 71
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Bromealin signal sequence

<400> 71
 atggcctgga aggtgcaggt ggtgttcctc ttcctcttcc tctgcgtgat gtgggcctcc 60
 ccgtccgccg cctccgcc 78

<210> 72
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Bromealin signal peptide

<400> 72

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala
20 25

<210> 73
<211> 1050
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN11000

<400> 73
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atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgccg cttccagatc 180
ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctctacacc 240
ctcggcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc 300
ggcatctccc gcccgctcaa catcgagcgc gagccggtgg tgtccttcga cgacgtggac 360
atctccgccg tgccgcagtc catcgactgg cgcgactacg gcgccgtgac ctccgtgaag 420
aaccagaacc cgtgcggcgc ctgctggggc ttccgcccca tcgccaccgt ggagtccatc 480
tacaagatca agaagggcat cctcgagccg ctctccgagc agcaggtgct cgactgcgcc 540
aagggctacg gctgcaaggg cggctgggag ttccgcgcct tcgagttcat catctccaac 600
aagggcgtgg cctccggcgc catctacccg tacaaggccg ccaagggcac ctgcaagacc 660
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tcctccatga tgtacgccgt gtccaagcag ccgatcaccg tggccgtgga cgccaacgcc 780
aacttccagt actacaagtc cggcgtgttc aacggcccgt gcggcacctc cctcaaccac 840
gccgtgaccg ccatcggcta cggccaggac tccatcatct acccgaagaa gtggggcgcc 900
aagtggggcg aggccggcta catccgcatg gcccgcgacg tgtcctcctc ctccggcatc 960
tgcggcatcg ccatcgaccc gctctacccg accctcgagg aggtgttcgc cgaggccatc 1020
gccgccaact ccaccctcgt ggccgagtag 1050

<210> 74
<211> 1067
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN11589

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<400> 74

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ccgaccgcgc cgcctccacc gacgagccgt ccgacccgat gatgaagcgc ttcgaggagt	180
ggatggtgga gtacggccgc gtgtacaagg acaacgacga gaagatgcgc cgcttccaga	240
tcttcaagaa caacgtgaac cacatcgaga ccttcaactc ccgcaacgag aactcctaca	300
ccctcggcat caaccagttc accgacatga ccaacaacga gttcatcgcc cagtacaccg	360
gcggcatctc ccgcccgcctc aacatcgagc gcgagccggt ggtgtccttc gacgacgtgg	420
acatctccgc cgtgccgcag tccatcgact ggcgcgacta cggcgccgtg acctccgtga	480
agaaccagaa cccgtgcggc gcctgctggg ccttcgccgc catcgccacc gtggagtcca	540
tctacaagat caagaagggc atcctcgagc cgctctccga gcagcaggtg ctcgactgcg	600
ccaagggcta cggctgcaag ggcggctggg agttccgcgc cttcgagtcc atcatctcca	660
acaagggcgt ggcctccggc gccatctacc cgtacaaggc cgccaagggc acctgcaaga	720
ccgacggcgt gccgaactcc gcctacatca ccggctacgc ccgcggtgccg cgcaacaacg	780
agtcctccat gatgtacgcc gtgtccaagc agccgatcac cgtggccgtg gacgccaacg	840
ccaacttcca gtactacaag tccggcgtgt tcaacggccc gtgcggcacc tccctcaacc	900
acgccgtgac cgccatcggc tacggccagg actccatcat ctacccgaag aagtggggcg	960
ccaagtgggg cgaggccggc tacatccgca tggcccgcga cgtgtcctcc tcctccggca	1020
tctgcggcat cgccatcgac ccgctctacc cgaccctcga ggagtag	1067

<210> 75

<211> 1023

<212> DNA

<213> Artificial Sequence

<220>

<223> pSYN11587 Sequence

<400> 75

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ccgtccgccg cctccgcgga cgagccgtcc gacccgatga tgaagcgctt cgaggagtgg	120
atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgccg cttccagatc	180
ttcaagaaca acgtgaacca catcgagacc tteaactccc gcaacgagaa ctctacacc	240
ctcggcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc	300
ggcatctccc gcccgctcaa catcgagcgc gagccggtgg tgtccttcga cgacgtggac	360
atctccgccg tgccgcagtc catcgactgg cgcgactacg gcgccgtgac ctccgtgaag	420
aaccagaacc cgtgcggcgc ctgctgggcc ttccgcccca tcgccaccgt ggagtccatc	480

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tacaagatca	agaagggcat	cctcgagccg	ctctccgagc	agcaggtgct	cgactgcgcc	540
aagggctacg	gctgcaaggg	cggctgggag	ttccgcgctt	tcgagttcat	catctccaac	600
aagggcgtgg	cctccggcgc	catctacccg	tacaaggccg	ccaagggcac	ctgcaagacc	660
gacggcgtgc	cgaactccgc	ctacatcacc	ggctacgccc	gcgtgccgcg	caacaacgag	720
tcctccatga	tgtacgccgt	gtccaagcag	ccgatcaccg	tggccgtgga	cgccaacgcc	780
aacttccagt	actacaagtc	cggcgtgttc	aacggcccgt	gcggcacctc	cctcaaccac	840
gccgtgaccg	ccatcggcta	cggccaggac	tccatcatct	acccgaagaa	gtggggcgcc	900
aagtggggcg	aggccggcta	catccgcatg	gcccgcgacg	tgtcctcctc	ctccggcatc	960
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tag						1023

<210> 76
 <211> 990
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN12169 Sequence

<400> 76		
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cgcgtgtaca	aggacaacga cgagaagatg cgccgcttcc agatcttcaa gaacaacgtg 180	
aaccacatcg	agaccttcaa ctcccgaac gagaactcct acaccctcgg catcaaccag 240	
ttcaccgaca	tgaccaacaa cgagttcatc gcccagtaca ccggcgggcat ctcccgcccg 300	
ctcaacatcg	agcgcgagcc ggtggtgtcc ttcgacgacg tggacatctc cgccgtgccg 360	
cagtccatcg	actggcgcgga ctacggcgcc gtgacctccg tgaagaacca gaacccgtgc 420	
ggcgcttgc	gggccttcgc cgccatcgcc accgtggagt ccatctacaa gatcaagaag 480	
ggcatcctcg	agccgctctc cgagcagcag gtgctcgact gcgccaaggg ctacggctgc 540	
aagggcggct	gggagttccg cgccttcgag ttcatcatct ccaacaaggg cgtggcctcc 600	
ggcgccatct	acccgtacaa ggccgccaag ggcacctgca agaccgacgg cgtgccgaac 660	
tccgcctaca	tcaccggcta cgcccgcgtg ccgcgcaaca acgagtcctc catgatgtac 720	
gccgtgtcca	agcagccgat caccgtggcc gtggacgcca acgccaactt ccagtactac 780	
aagtccggcg	tgttcaacgg cccgtgcggc acctccctca accacgccgt gaccgccatc 840	
ggctacggcc	aggactccat catctacccg aagaagtggg gcgccaagtg gggcgaggcc 900	
ggctacatcc	gcatggcccc cgacgtgtcc tcctcctccg gcatctgcgg catcgccatc 960	
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

<210> 77
 <211> 1170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN12575 Sequence

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 gcggcggaca cgctcagcat gcggaccagc gcgcgcgcgg cggccaggca ccagcaccag 180
 cagggcgccc gcggggccag gttcccgtcg ctcgtcgtgt gcgccagcgc cggcgccatg 240
 gcggacgagc cgtccgaccc gatgatgaag cgcttcgagg agtggatggg ggagtacggc 300
 cgcgtgtaca aggacaacga cgagaagatg cgccgcttcc agatcttcaa gaacaacgtg 360
 aaccacatcg agaccttcaa ctcccgaac gagaactcct acaccctcgg catcaaccag 420
 ttcaccgaca tgaccaacaa cgagttcatc gcccagtaca ccggcgggcat ctcccggccg 480
 ctcaacatcg agcgcgagcc ggtggtgtcc ttcgacgacg tggacatctc cgccgtgccg 540
 cagtccatcg actggcgcgga ctacggcgcc gtgacctccg tgaagaacca gaaccctgtc 600
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 ggcatcctcg agccgctctc cgagcagcag gtgctcgact gcgccaaggg ctacggctgc 720
 aagggcggct gggagttccg cgccttcgag ttcatcatct ccaacaaggg cgtggcctcc 780
 ggcgccatct acccgtaaa ggccgccaag ggcacctgca agaccgacgg cgtgccgaac 840
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 gccgtgtcca agcagccgat caccgtggcc gtggacgcca acgccaactt ccagtactac 960
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<210> 78
 <211> 1068
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSM270 Sequence

<400> 78
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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tggatggtgg agtacggccg cgtgtacaag gacaacgacg agaagatgcg ccgcttccag 240
atcttcaaga acaacgtgaa ccacatcgag accttcaact cccgcaacga gaactcctac 300
accctcggca tcaaccagtt caccgacatg accaacaacg agttcatcgc ccagtacacc 360
ggcggcatct cccgcccgtc caacatcgag cgcgagccgg tgggtgtcctt cgacgacgtg 420
gacatctccg ccgtgccgca gtccatcgac tggcgcgact acggcgcgct gacctccgtg 480
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gccaagggct acggctgcaa gggcggctgg gagttccgcg ccttcgagtt catcatctcc 660
aacaagggcg tggcctccgg cgccatctac ccgtacaagg ccgccaaggg cacctgcaag 720
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cacgccgtga ccgccatcgg ctacggccag gactccatca tctacccgaa gaagtggggc 960
gccaagtggg gcgaggccgg ctacatccgc atggcccgcg acgtgtcctc ctctccggc 1020
atctgcggca tcgccatcga cccgctctac ccgaccctcg aggagtag 1068

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<210> 79
<211> 1497
<212> DNA
<213> Trichoderma reesei

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<220>
<221> CDS
<222> (1)..(1497)
<223> Trichoderma reesei cellobiohydrolase I

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<400> 79
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1 5 10 15

tgg cag aaa tgc tcg tct ggt ggc acg tgc act caa cag aca ggc tcc 96
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
20 25 30

gtg gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac agc agc 144
Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
35 40 45

acg aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt cct gac 192
Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
50 55 60

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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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tcc Ser	acg Thr	tac Tyr	gga Gly	ggt Val 85	acc Thr	acg Thr	agc Ser	ggc Gly	aac Asn 90	agc Ser	ctc Leu	tcc Ser	att Ile	ggc Gly 95	ttt Phe	288
gtc Val	acc Thr	cag Gln	tct Ser 100	gag Ala	cag Gln	aag Lys	aac Asn	ggt Val 105	ggc Gly	gct Ala	cgc Arg	ctt Leu	tac Tyr 110	ctt Leu	atg Met	336
gag Ala	agc Ser	gac Asp 115	acg Thr	acc Thr	tac Tyr	cag Gln	gaa Glu 120	ttc Phe	acc Thr	ctg Leu	ctt Leu	ggc Gly 125	aac Asn	gag Glu	ttc Phe	384
tct Ser	ttc Phe 130	gat Asp	ggt Val	gat Asp	ggt Val	tcg Ser 135	cag Gln	ctg Leu	ccg Pro	tgc Cys	ggc Gly 140	ttg Leu	aac Asn	gga Gly	gct Ala	432
ctc Leu 145	tac Tyr	ttc Phe	gtg Val	tcc Ser	atg Met 150	gac Asp	gag Ala	gat Asp	ggc Gly	gtg Val	agc Ser	aag Lys	tat Tyr	ccc Pro 160		480
acc Thr	aac Asn	acc Thr	gct Ala	ggc Gly 165	gcc Ala	aag Lys	tac Tyr	ggc Gly	acg Thr 170	ggg Gly	tac Tyr	tgt Cys	gac Asp	agc Ser 175	cag Gln	528
tgt Cys	ccc Pro	cgc Arg	gat Asp 180	ctg Leu	aag Lys	ttc Phe	atc Ile	aat Asn 185	ggc Gly	cag Gln	gcc Ala	aac Asn	ggt Val 190	gag Glu	ggc Gly	576
tgg Trp	gag Glu	ccg Pro 195	tca Ser	tcc Ser	aac Asn	aac Asn	gag Ala 200	aac Asn	acg Thr	ggc Gly	att Ile	gga Gly 205	gga Gly	cac His	gga Gly	624
agc Ser	tgc Cys 210	tgc Cys	tct Ser	gag Glu	atg Met	gat Asp 215	atc Ile	tgg Trp	gag Glu	gcc Ala	aac Asn 220	tcc Ser	atc Ile	tcc Ser	gag Glu	672
gct Ala 225	ctt Leu	acc Thr	ccc Pro	cac His	cct Pro 230	tgc Cys	acg Thr	act Thr	gtc Val	ggc Gly 235	cag Gln	gag Glu	atc Ile	tgc Cys	gag Glu 240	720
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tgc Cys	gat Asp	ccc Pro	gat Asp 260	ggc Gly	tgc Cys	gac Asp	tgg Trp	aac Asn 265	cca Pro	tac Tyr	cgc Arg	ctg Leu	ggc Gly 270	aac Asn	acc Thr	816
agc Ser	ttc Phe	tac Tyr 275	ggc Gly	cct Pro	ggc Gly	tct Ser	agc Ser 280	ttt Phe	acc Thr	ctc Leu	gat Asp	acc Thr 285	acc Thr	aag Lys	aaa Lys	864
ttg Leu	acc Thr 290	ggt Val	gtc Val	acc Thr	cag Gln	ttc Phe 295	gag Glu	acg Thr	tcg Ser	ggc Gly	gcc Ala 300	atc Ile	aac Asn	cga Arg	tac Tyr	912
tat Tyr 305	gtc Val	cag Gln	aat Asn	ggc Gly	gtc Val 310	act Thr	ttc Phe	cag Gln	cag Gln	ccc Pro 315	aac Asn	gcc Ala	gag Glu	ctt Leu	ggc Gly 320	960

60110USPCT1 Corrected SEQ LIST 2-2007.txt

agt tac tct ggc aac gag ctc aac gat gat tac tgc aca gct gag gag	1008
Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu	
325 330 335	
gca gaa ttc ggc gga tcc tct ttc tca gac aag ggc ggc ctg act cag	1056
Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln	
340 345 350	
ttc aag aag gct acc tct ggc ggc atg gtt ctg gtc atg agt ctg tgg	1104
Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp	
355 360 365	
gat gat tac tac gcc aac atg ctg tgg ctg gac tcc acc tac ccg aca	1152
Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr	
370 375 380	
aac gag acc tcc tcc aca ccc ggt gcc gtg cgc gga agc tgc tcc acc	1200
Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr	
385 390 395 400	
agc tcc ggt gtc cct gct cag gtc gaa tct cag tct ccc aac gcc aag	1248
Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys	
405 410 415	
gtc acc ttc tcc aac atc aag ttc gga ccc att ggc agc acc ggc aac	1296
Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn	
420 425 430	
cct agc ggc ggc aac cct ccc ggc gga aac ccg cct ggc acc acc acc	1344
Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr	
435 440 445	
acc cgc cgc cca gcc act acc act gga agc tct ccc gga cct acc cag	1392
Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln	
450 455 460	
tct cac tac ggc cag tgc ggc ggt att ggc tac agc ggc ccc acg gtc	1440
Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val	
465 470 475 480	
tgc gcc agc ggc aca act tgc cag gtc ctg aac cct tac tac tct cag	1488
Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln	
485 490 495	
tgc ctg taa	1497
Cys Leu	

<210> 80
 <211> 498
 <212> PRT
 <213> Trichoderma reesei

<400> 80

Met Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
1 5 10 15

Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
20 25 30

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
35 40 45

Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
50 55 60

Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
65 70 75 80

Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
85 90 95

Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
100 105 110

Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
115 120 125

Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
130 135 140

Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
145 150 155 160

Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
165 170 175

Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
180 185 190

Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
195 200 205

Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
210 215 220

Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
225 230 235 240

Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
245 250 255

Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
260 265 270

Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys

275

280

285

Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
290 295 300

Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
305 310 315 320

Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
325 330 335

Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
340 345 350

Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
355 360 365

Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
370 375 380

Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
385 390 395 400

Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
405 410 415

Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
420 425 430

Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
435 440 445

Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
450 455 460

Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
465 470 475 480

Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
485 490 495

Cys Leu

<210> 81
<211> 1365
<212> DNA
<213> Trichoderma reesei

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>

<221> CDS

<222> (1)..(1365)

<223> trichoderma reesei cellobiohydrolase II

<400> 81

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Met	Val	Pro	Leu	Glu	Glu	Arg	Gln	Ala	Cys	Ser	Ser	Val	Trp	Gly	Gln	
1				5					10					15		

tgt	ggt	ggc	cag	aat	tgg	tcg	ggt	ccg	act	tgc	tgt	gct	tcc	gga	agc	96
Cys	Gly	Gly	Gln	Asn	Trp	Ser	Gly	Pro	Thr	Cys	Cys	Ala	Ser	Gly	Ser	
			20					25					30			

aca	tgc	gtc	tac	tcc	aac	gac	tat	tac	tcc	cag	tgt	ctt	ccc	ggc	gct	144
Thr	Cys	Val	Tyr	Ser	Asn	Asp	Tyr	Tyr	Ser	Gln	Cys	Leu	Pro	Gly	Ala	
		35					40					45				

gca	agc	tca	agc	tcg	tcc	acg	cgc	gcc	gcg	tcg	acg	act	tca	cga	gta	192
Ala	Ser	Ser	Ser	Ser	Ser	Thr	Arg	Ala	Ala	Ser	Thr	Thr	Ser	Arg	Val	
	50					55					60					

tcc	ccc	aca	aca	tcc	cgg	tcg	agc	tcc	gcg	acg	cct	cca	cct	ggt	tct	240
Ser	Pro	Thr	Thr	Ser	Arg	Ser	Ser	Ser	Ala	Thr	Pro	Pro	Pro	Gly	Ser	
65					70					75					80	

acc	act	acc	aga	gta	cct	cca	gtc	gga	tcg	gga	acc	gct	acg	tat	tca	288
Thr	Thr	Thr	Arg	Val	Pro	Pro	Val	Gly	Ser	Gly	Thr	Ala	Thr	Tyr	Ser	
				85					90					95		

ggc	aac	cct	ttt	gtt	ggg	gtc	act	cct	tgg	gcc	aat	gca	tat	tac	gcc	336
Gly	Asn	Pro	Phe	Val	Gly	Val	Thr	Pro	Trp	Ala	Asn	Ala	Tyr	Tyr	Ala	
			100					105					110			

tct	gaa	gtt	agc	agc	ctc	gct	att	cct	agc	ttg	act	gga	gcc	atg	gcc	384
Ser	Glu	Val	Ser	Ser	Leu	Ala	Ile	Pro	Ser	Leu	Thr	Gly	Ala	Met	Ala	
		115					120					125				

act	gct	gca	gca	gct	gtc	gca	aag	gtt	ccc	tct	ttt	atg	tgg	cta	gat	432
Thr	Ala	Ala	Ala	Ala	Val	Ala	Lys	Val	Pro	Ser	Phe	Met	Trp	Leu	Asp	
	130					135					140					

act	ctt	gac	aag	acc	cct	ctc	atg	gag	caa	acc	ttg	gcc	gac	atc	cgc	480
Thr	Leu	Asp	Lys	Thr	Pro	Leu	Met	Glu	Gln	Thr	Leu	Ala	Asp	Ile	Arg	
145					150					155					160	

acc	gcc	aac	aag	aat	ggc	ggt	aac	tat	gcc	gga	cag	ttt	gtg	gtg	tat	528
Thr	Ala	Asn	Lys	Asn	Gly	Gly	Asn	Tyr	Ala	Gly	Gln	Phe	Val	Val	Tyr	
				165					170				175			

gac	ttg	ccg	gat	cgc	gat	tgc	gct	gcc	ctt	gcc	tcg	aat	ggc	gaa	tac	576
Asp	Leu	Pro	Asp	Arg	Asp	Cys	Ala	Ala	Leu	Ala	Ser	Asn	Gly	Glu	Tyr	
			180					185					190			

tct	att	gcc	gat	ggt	ggc	gtc	gcc	aaa	tat	aag	aac	tat	atc	gac	acc	624
Ser	Ile	Ala	Asp	Gly	Gly	Val	Ala	Lys	Tyr	Lys	Asn	Tyr	Ile	Asp	Thr	
		195					200					205				

att	cgt	caa	att	gtc	gtg	gaa	tat	tcc	gat	atc	cgg	acc	ctc	ctg	gtt	672
Ile	Arg	Gln	Ile	Val	Val	Glu	Tyr	Ser	Asp	Ile	Arg	Thr	Leu	Leu	Val	
	210					215					220					

60110USPCT1 Corrected SEQ LIST 2-2007.txt

att Ile 225	gag Glu	cct Pro	gac Asp	tct Ser	ctt Leu 230	gcc Ala	aac Asn	ctg Leu	gtg Val	acc Thr 235	aac Asn	ctc Leu	ggt Gly	act Thr	cca Pro 240	720
aag Lys	tgt Cys	gcc Ala	aat Asn	gct Ala 245	cag Gln	tca Ser	gcc Ala	tac Tyr	ctt Leu 250	gag Glu	tgc Cys	atc Ile	aac Asn	tac Tyr 255	gcc Ala	768
gtc Val	aca Thr	cag Gln	ctg Leu 260	aac Asn	ctt Leu	cca Pro	aat Asn	gtt Val 265	gcg Ala	atg Met	tat Tyr	ttg Leu	gac Asp 270	gct Ala	ggc Gly	816
cat His	gca Ala	gga Gly 275	tgg Trp	ctt Leu	ggc Gly	tgg Trp	ccg Pro 280	gca Ala	aac Asn	caa Gln	gac Asp	ccg Pro 285	gcc Ala	gct Ala	cag Gln	864
cta Leu	ttt Phe 290	gca Ala	aat Asn	gtt Val	tac Tyr	aag Lys 295	aat Asn	gca Ala	tcg Ser	tct Ser	ccg Pro 300	aga Arg	gct Ala	ctt Leu	cgc Arg	912
gga Gly 305	ttg Leu	gca Ala	acc Thr	aat Asn	gtc Val 310	gcc Ala	aac Asn	tac Tyr	aac Asn	ggg Gly 315	tgg Trp	aac Asn	att Ile	acc Thr	agc Ser 320	960
ccc Pro	cca Pro	tcg Ser	tac Tyr	acg Thr 325	caa Gln	ggc Gly	aac Asn	gct Ala	gtc Val 330	tac Tyr	aac Asn	gag Glu	aag Lys	ctg Leu 335	tac Tyr	1008
atc Ile	cac His	gct Ala	att Ile 340	gga Gly	cct Pro	ctt Leu	ctt Leu	gcc Ala 345	aat Asn	cac His	ggc Gly	tgg Trp	tcc Ser 350	aac Asn	gcc Ala	1056
ttc Phe	ttc Phe	atc Ile 355	act Thr	gat Asp	caa Gln	ggt Gly	cga Arg 360	tcg Ser	gga Gly	aag Lys	cag Gln	cct Pro 365	acc Thr	gga Gly	cag Gln	1104
caa Gln 370	cag Gln	tgg Trp	gga Gly	gac Asp	tgg Trp	tgc Cys 375	aat Asn	gtg Val	atc Ile	ggc Gly	acc Thr 380	gga Gly	ttt Phe	ggt Gly	att Ile	1152
cgc Arg 385	cca Pro	tcc Ser	gca Ala	aac Asn	act Thr 390	ggg Gly	gac Asp	tcg Ser	ttg Leu	ctg Leu 395	gat Asp	tcg Ser	ttt Phe	gtc Val	tgg Trp 400	1200
gtc Val	aag Lys	cca Pro	ggc Gly	ggc Gly 405	gag Glu	tgt Cys	gac Asp	ggc Gly	acc Thr 410	agc Ser	gac Asp	agc Ser	agt Ser	gcg Ala 415	cca Pro	1248
cga Arg	ttt Phe	gac Asp	tcc Ser 420	cac His	tgt Cys	gcg Ala	ctc Leu	cca Pro 425	gat Asp	gcc Ala	ttg Leu	caa Gln	ccg Pro 430	gcg Ala	cct Pro	1296
caa Gln	gct Ala	ggt Gly 435	gct Ala	tgg Trp	ttc Phe	caa Gln	gcc Ala 440	tac Tyr	ttt Phe	gtg Val	cag Gln	ctt Leu 445	ctc Leu	aca Thr	aac Asn	1344
gca Ala 450	aac Asn	cca Pro	tcg Ser	ttc Phe	ctg Leu	tag										1365

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<211> 454

<212> PRT

<213> Trichoderma reesei

<400> 82

Met Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly Gln
1 5 10 15

Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser
20 25 30

Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala
35 40 45

Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val
50 55 60

Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser
65 70 75 80

Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser
85 90 95

Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala
100 105 110

Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala
115 120 125

Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp
130 135 140

Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg
145 150 155 160

Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr
165 170 175

Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr
180 185 190

Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr
195 200 205

Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val
210 215 220

Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro
Page 78

225

230

235

240

Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala
245 250 255

Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly
260 265 270

His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln
275 280 285

Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg
290 295 300

Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser
305 310 315 320

Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr
325 330 335

Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala
340 345 350

Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln
355 360 365

Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile
370 375 380

Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp
385 390 395 400

Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro
405 410 415

Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro
420 425 430

Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn
435 440 445

Ala Asn Pro Ser Phe Leu
450

<210> 83

<211> 1317

<212> DNA

<213> Trichoderma reesei

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>

<221> CDS

<222> (1)..(1317)

<223> Trichoderma reesei endoglucanase I

<400> 83

atg	cag	caa	ccg	gga	acc	agc	acc	ccc	gag	gtc	cat	ccc	aag	ttg	aca	48
Met	Gln	Gln	Pro	Gly	Thr	Ser	Thr	Pro	Glu	Val	His	Pro	Lys	Leu	Thr	
1				5					10					15		

acc	tac	aag	tgc	aca	aag	tcc	ggg	ggg	tgc	gtg	gcc	cag	gac	acc	tgc	96
Thr	Tyr	Lys	Cys	Thr	Lys	Ser	Gly	Gly	Cys	Val	Ala	Gln	Asp	Thr	Ser	
			20					25					30			

gtg	gtc	ctt	gac	tgg	aac	tac	cgc	tgg	atg	cac	gac	gca	aac	tac	aac	144
Val	Val	Leu	Asp	Trp	Asn	Tyr	Arg	Trp	Met	His	Asp	Ala	Asn	Tyr	Asn	
		35					40					45				

tcg	tgc	acc	gtc	aac	ggc	ggc	gtc	aac	acc	acg	ctc	tgc	cct	gac	gag	192
Ser	Cys	Thr	Val	Asn	Gly	Gly	Val	Asn	Thr	Thr	Leu	Cys	Pro	Asp	Glu	
	50					55					60					

gcg	acc	tgt	ggc	aag	aac	tgc	ttc	atc	gag	ggc	gtc	gac	tac	gcc	gcc	240
Ala	Thr	Cys	Gly	Lys	Asn	Cys	Phe	Ile	Glu	Gly	Val	Asp	Tyr	Ala	Ala	
65					70					75					80	

tcg	ggc	gtc	acg	acc	tcg	ggc	agc	agc	ctc	acc	atg	aac	cag	tac	atg	288
Ser	Gly	Val	Thr	Thr	Ser	Gly	Ser	Ser	Leu	Thr	Met	Asn	Gln	Tyr	Met	
				85					90					95		

ccc	agc	agc	tct	ggc	ggc	tac	agc	agc	gtc	tct	cct	cgg	ctg	tat	ctc	336
Pro	Ser	Ser	Ser	Gly	Gly	Tyr	Ser	Ser	Val	Ser	Pro	Arg	Leu	Tyr	Leu	
			100					105					110			

ctg	gac	tct	gac	ggt	gag	tac	gtg	atg	ctg	aag	ctc	aac	ggc	cag	gag	384
Leu	Asp	Ser	Asp	Gly	Glu	Tyr	Val	Met	Leu	Lys	Leu	Asn	Gly	Gln	Glu	
		115					120					125				

ctg	agc	ttc	gac	gtc	gac	ctc	tct	gct	ctg	ccg	tgt	gga	gag	aac	ggc	432
Leu	Ser	Phe	Asp	Val	Asp	Leu	Ser	Ala	Leu	Pro	Cys	Gly	Glu	Asn	Gly	
	130					135					140					

tcg	ctc	tac	ctg	tct	cag	atg	gac	gag	aac	ggg	ggc	gcc	aac	cag	tat	480
Ser	Leu	Tyr	Leu	Ser	Gln	Met	Asp	Glu	Asn	Gly	Gly	Ala	Asn	Gln	Tyr	
145					150					155					160	

aac	acg	gcc	ggt	gcc	aac	tac	ggg	agc	ggc	tac	tgc	gat	gct	cag	tgc	528
Asn	Thr	Ala	Gly	Ala	Asn	Tyr	Gly	Ser	Gly	Tyr	Cys	Asp	Ala	Gln	Cys	
				165					170					175		

ccc	gtc	cag	aca	tgg	agg	aac	ggc	acc	ctc	aac	act	agc	cac	cag	ggc	576
Pro	Val	Gln	Thr	Trp	Arg	Asn	Gly	Thr	Leu	Asn	Thr	Ser	His	Gln	Gly	
			180					185					190			

ttc	tgc	tgc	aac	gag	atg	gat	atc	ctg	gag	ggc	aac	tcg	agg	gcg	aat	624
Phe	Cys	Cys	Asn	Glu	Met	Asp	Ile	Leu	Glu	Gly	Asn	Ser	Arg	Ala	Asn	
		195					200					205				

gcc	ttg	acc	cct	cac	tct	tgc	acg	gcc	acg	gcc	tgc	gac	tct	gcc	ggt	672
Ala	Leu	Thr	Pro	His	Ser	Cys	Thr	Ala	Thr	Ala	Cys	Asp	Ser	Ala	Gly	
	210					215					220					

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tgc Cys 225	ggc Gly	ttc Phe	aac Asn	ccc Pro	tat Tyr 230	ggc Gly	agc Ser	ggc Gly	tac Tyr	aaa Lys 235	agc Ser	tac Tyr	tac Tyr	ggc Gly	ccc Pro 240	720
gga Gly	gat Asp	acc Thr	gtt Val	gac Asp 245	acc Thr	tcc Ser	aag Lys	acc Thr	ttc Phe 250	acc Thr	atc Ile	atc Ile	acc Thr	cag Gln 255	ttc Phe	768
aac Asn	acg Thr	gac Asp	aac Asn 260	ggc Gly	tcg Ser	ccc Pro	tcg Ser	ggc Gly 265	aac Asn	ctt Leu	gtg Val	agc Ser	atc Ile 270	acc Thr	cgc Arg	816
aag Lys	tac Tyr	cag Gln 275	caa Gln	aac Asn	ggc Gly	gtc Val	gac Asp 280	atc Ile	ccc Pro	agc Ser	gcc Ala	cag Gln 285	ccc Pro	ggc Gly	ggc Gly	864
gac Asp	acc Thr 290	atc Ile	tcg Ser	tcc Ser	tgc Cys	ccg Pro 295	tcc Ser	gcc Ala	tca Ser	gcc Ala	tac Tyr 300	ggc Gly	ggc Gly	ctc Leu	gcc Ala	912
acc Thr 305	atg Met	ggc Gly	aag Lys	gcc Ala	ctg Leu 310	agc Ser	agc Ser	ggc Gly	atg Met	gtg Val 315	ctc Leu	gtg Val	ttc Phe	agc Ser	att Ile 320	960
tgg Trp	aac Asn	gac Asp	aac Asn	agc Ser 325	cag Gln	tac Tyr	atg Met	aac Asn	tgg Trp 330	ctc Leu	gac Asp	agc Ser	ggc Gly	aac Asn 335	gcc Ala	1008
ggc Gly	ccc Pro	tgc Cys	agc Ser 340	agc Ser	acc Thr	gag Glu	ggc Gly	aac Asn 345	cca Pro	tcc Ser	aac Asn	acc Thr	ctg Leu 350	gcc Ala	aac Asn	1056
aac Asn	ccc Pro	aac Asn 355	acg Thr	cac His	gtc Val	gtc Val	ttc Phe 360	tcc Ser	aac Asn	atc Ile	cgc Arg	tgg Trp 365	gga Gly	gac Asp	att Ile	1104
ggg Gly	tct Ser 370	act Thr	acg Thr	aac Asn	tcg Ser	act Thr 375	gcg Ala	ccc Pro	ccg Pro	ccc Pro	ccg Pro 380	cct Pro	gcg Ala	tcc Ser	agc Ser	1152
acg Thr 385	acg Thr	ttt Phe	tcg Ser	act Thr	aca Thr 390	cgg Arg	agg Arg	agc Ser	tcg Ser	acg Thr 395	act Thr	tcg Ser	agc Ser	agc Ser	ccg Pro 400	1200
agc Ser	tgc Cys	acg Thr	cag Gln	act Thr 405	cac His	tgg Trp	ggg Gly	cag Gln	tgc Cys 410	ggt Gly	ggc Gly	att Ile	ggg Gly	tac Tyr 415	agc Ser	1248
ggg Gly	tgc Cys	aag Lys	acg Thr 420	tgc Cys	acg Thr	tcg Ser	ggc Gly	act Thr 425	acg Thr	tgc Cys	cag Gln	tat Tyr	agc Ser 430	aac Asn	gac Asp	1296
tac Tyr	tac Tyr	tcg Ser	caa Gln	tgc Cys	ctt Leu	tag										1317

<210> 84
 <211> 438
 <212> PRT
 <213> Trichoderma reesei

<400> 84

Met Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr
1 5 10 15

Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser
20 25 30

Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
35 40 45

Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
50 55 60

Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
65 70 75 80

Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
85 90 95

Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu
100 105 110

Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
115 120 125

Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly
130 135 140

Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
145 150 155 160

Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
165 170 175

Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
180 185 190

Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
195 200 205

Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
210 215 220

Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
225 230 235 240

Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe

Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
260 265 270

Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
275 280 285

Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
290 295 300

Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
305 310 315 320

Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
325 330 335

Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn
340 345 350

Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
355 360 365

Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
370 375 380

Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
385 390 395 400

Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
405 410 415

Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
420 425 430

Tyr Tyr Ser Gln Cys Leu
435

<210> 85
<211> 954
<212> DNA
<213> Artificial Sequence

<220>
<223> 6GP1

<220>
<221> CDS
<222> (1)..(954)

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<223> 6GP1

<400> 85

atg ggc gtg gac ccg ttc gag cgc aac aag atc ctc ggc cgc ggc atc	48
Met Gly Val Asp Pro Phe Glu Arg Asn Lys Ile Leu Gly Arg Gly Ile	
1 5 10 15	
aac atc ggc aac gcc ctg gag gcc ccg aac gag ggc gac tgg ggc gtg	96
Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val	
20 25 30	
gtg atc aag gac gag ttc ttc gac atc atc aag gag gcc ggc ttc tcc	144
Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser	
35 40 45	
cac gtg cgc atc ccg atc cgc tgg tcc acc cac gcc tac gcc ttc ccg	192
His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro	
50 55 60	
ccg tac aag atc atg gac cgc ttc ttc aag cgc gtg gac gag gtg atc	240
Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile	
65 70 75 80	
aac ggc gcc ctc aag cgc ggc ctc gcc gtg gcc atc aac atc cac cac	288
Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His	
85 90 95	
tac gag gag ctc atg aac gac ccg gag gag cac aag gag cgc ttc ctc	336
Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu	
100 105 110	
gcc ctc tgg aag cag atc gcc gac cgc tac aag gac tac ccg gag acc	384
Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr	
115 120 125	
ctc ttc ttc gag atc ctc aac gag ccg cac ggc aac ctc acc ccg gag	432
Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu	
130 135 140	
aag tgg aac gag ctg ctc gag gag gcc ctc aag gtg atc cgc tcc atc	480
Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile	
145 150 155 160	
gac aag aag cac acc atc atc att ggc acc gca gag tgg gga ggc atc	528
Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile	
165 170 175	
tcc gcc ctc gag aag ctc tcc gtg ccg aag tgg gag aag aat tcc atc	576
Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile	
180 185 190	
gtg acc atc cac tac tac aac ccg ttc gag ttc acg cac cag ggc gcc	624
Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala	
195 200 205	
gag tgg gtg gag ggc tcc gag aag tgg ctt ggc cgc aag tgg ggc tcc	672
Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser	
210 215 220	
ccg gac gac cag aag cac ctc atc gag gag ttc aac ttc atc gag gag	720
Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu	
225 230 235 240	

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tgg tcc aag aag aac aag cgc ccg atc tac atc ggc gag ttt ggc gcc	768
Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala	
245 250 255	
tac cgc aag gcc gac ctc gag tcc cgc atc aag tgg acc tcc ttc gtg	816
Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val	
260 265 270	
gtg cgt gag atg gag aag cgc cgc tgg tcc tgg gcc tac tgg gag ttc	864
Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe	
275 280 285	
tgc tcc ggc ttc ggc gtg tac gac acc ctc cgc aag acc tgg aac aag	912
Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys	
290 295 300	
gac ctc ctc gag gcc ctc atc ggc ggc gac tcc atc gag tag	954
Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu	
305 310 315	

<210> 86
 <211> 317
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 86

Met Gly Val Asp Pro Phe Glu Arg Asn Lys Ile Leu Gly Arg Gly Ile	
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20 25 30	
Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser	
35 40 45	
His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro	
50 55 60	
Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile	
65 70 75 80	
Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His	
85 90 95	
Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu	
100 105 110	
Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr	
115 120 125	

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu
130 135 140

Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile
145 150 155 160

Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile
165 170 175

Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile
180 185 190

Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala
195 200 205

Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser
210 215 220

Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu
225 230 235 240

Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala
245 250 255

Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val
260 265 270

Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe
275 280 285

Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys
290 295 300

Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu
305 310 315

<210> 87
<211> 1248
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (1)..(1248)
<223> Barley AmyI amylase

<400> 87
atg gca cac caa gtc ctc ttt cag ggg ttc aac tgg gag tcg tgg aag
Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
1 5 10 15

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cag Gln	agc Ser	ggc Gly	ggg Gly 20	tgg Trp	tac Tyr	aac Asn	atg Met	atg Met 25	atg Met	ggc Gly	aag Lys	gtc Val	gac Asp 30	gac Asp	atc Ile	96
gcc Ala	gct Ala	gcc Ala 35	gga Gly	gtc Val	acc Thr	cac His	gtc Val 40	tgg Trp	ctg Leu	cca Pro	ccg Pro	ccg Pro 45	tcg Ser	cac His	tcc Ser	144
gtc Val	tcc Ser 50	aac Asn	gaa Glu	ggt Gly	tac Tyr	atg Met 55	cct Pro	ggt Gly	cgg Arg	ctg Leu	tac Tyr 60	gac Asp	atc Ile	gac Asp	gcg Ala	192
tcc Ser 65	aag Lys	tac Tyr	ggc Gly	aac Asn	gcg Ala 70	gcg Ala	gag Glu	ctc Leu	aag Lys	tcg Ser 75	ctc Leu	atc Ile	ggc Gly	gcg Ala	ctc Leu 80	240
cac His	ggc Gly	aag Lys	ggc Gly	gtg Val 85	cag Gln	gcc Ala	atc Ile	gcc Ala	gac Asp 90	atc Ile	gtc Val	atc Ile	aac Asn	cac His 95	cgc Arg	288
tgc Cys	gcc Ala	gac Asp	tac Tyr 100	aag Lys	gat Asp	agc Ser	cgc Arg	ggc Gly 105	atc Ile	tac Tyr	tgc Cys	atc Ile	ttc Phe 110	gag Glu	ggc Gly	336
ggc Gly	acc Thr	tcc Ser 115	gac Asp	ggc Gly	cgc Arg	ctc Leu	gac Asp 120	tgg Trp	ggc Gly	ccc Pro	cac His	atg Met 125	atc Ile	tgt Cys	cgc Arg	384
gac Asp	gac Asp 130	acc Thr	aaa Lys	tac Tyr	tcc Ser	gat Asp 135	ggc Gly	acc Thr	gca Ala	aac Asn	ctc Leu 140	gac Asp	acc Thr	gga Gly	gcc Ala	432
gac Asp 145	ttc Phe	gcc Ala	gcc Ala	gcg Ala	ccc Pro 150	gac Asp	atc Ile	gac Asp	cac His	ctc Leu 155	aac Asn	gac Asp	cgg Arg	gtc Val	cag Gln 160	480
cgc Arg	gag Glu	ctc Leu	aag Lys	gag Glu 165	tgg Trp	ctc Leu	ctc Leu	tgg Trp	ctc Leu 170	aag Lys	agc Ser	gac Asp	ctc Leu	ggc Gly 175	ttc Phe	528
gac Asp	gcg Ala	tgg Trp	cgc Arg 180	ctt Leu	gac Asp	ttc Phe	gcc Ala	agg Arg 185	ggc Gly	tac Tyr	tcg Ser	ccg Pro	gag Glu 190	atg Met	gcc Ala	576
aag Lys	gtg Val	tac Tyr 195	atc Ile	gac Asp	ggc Gly	aca Thr	tcc Ser 200	ccg Pro	agc Ser	ctc Leu	gcc Ala	gtg Val 205	gcc Ala	gag Glu	gtg Val	624
tgg Trp	gac Asp 210	aat Asn	atg Met	gcc Ala	acc Thr	ggc Gly 215	ggc Gly	gac Asp	ggc Gly	aag Lys	ccc Pro 220	aac Asn	tac Tyr	gac Asp	cag Gln	672
gac Asp 225	gcg Ala	cac His	cgg Arg	cag Gln	aat Asn 230	ctg Leu	gtg Val	aac Asn	tgg Trp	gtg Val 235	gac Asp	aag Lys	gtg Val	ggc Gly	ggc Gly 240	720
gcg Ala	gcc Ala	tcg Ser	gca Ala	ggc Gly 245	atg Met	gtg Val	ttc Phe	gac Asp	ttc Phe 250	acg Thr	acc Thr	aaa Lys	ggg Gly	ata Ile 255	ctg Leu	768
aac Asn	gct Ala	gcc Ala	gtg Val	gag Glu	ggc Gly	gag Glu	ctg Leu	tgg Trp	agg Arg	ctg Leu	atc Ile	gac Asp	ccg Pro	cag Gln	ggg Gly	816

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260																265	270	
aag	gcc	ccc	ggc	gtg	atg	gga	tgg	tgg	ccg	gcc	aag	gcc	gtc	acc	ttc		864	
Lys	Ala	Pro	Gly	Val	Met	Gly	Trp	Trp	Pro	Ala	Lys	Ala	Val	Thr	Phe			
		275					280					285						
gtc	gac	aac	cac	gat	aca	ggc	tcc	acg	cag	gcc	atg	tgg	cca	ttc	ccc		912	
Val	Asp	Asn	His	Asp	Thr	Gly	Ser	Thr	Gln	Ala	Met	Trp	Pro	Phe	Pro			
	290					295					300							
tcc	gac	aag	gtc	atg	cag	ggc	tac	gcg	tac	atc	ctc	acc	cac	ccc	ggc		960	
Ser	Asp	Lys	Val	Met	Gln	Gly	Tyr	Ala	Tyr	Ile	Leu	Thr	His	Pro	Gly			
305					310					315					320			
atc	cca	tgc	atc	ttc	tac	gac	cat	ttc	ttc	aac	tgg	ggg	ttt	aag	gac		1008	
Ile	Pro	Cys	Ile	Phe	Tyr	Asp	His	Phe	Phe	Asn	Trp	Gly	Phe	Lys	Asp			
				325					330					335				
cag	atc	gcg	gcg	ctg	gtg	gcg	atc	agg	aag	cgc	aac	ggc	atc	acg	gcg		1056	
Gln	Ile	Ala	Ala	Leu	Val	Ala	Ile	Arg	Lys	Arg	Asn	Gly	Ile	Thr	Ala			
			340					345					350					
acg	agc	gct	ctg	aag	atc	ctc	atg	cac	gaa	gga	gat	gcc	tac	gtc	gcc		1104	
Thr	Ser	Ala	Leu	Lys	Ile	Leu	Met	His	Glu	Gly	Asp	Ala	Tyr	Val	Ala			
		355					360					365						
gag	ata	gac	ggc	aag	gtg	gtg	gtg	aag	atc	ggg	tcc	agg	tac	gac	gtc		1152	
Glu	Ile	Asp	Gly	Lys	Val	Val	Val	Lys	Ile	Gly	Ser	Arg	Tyr	Asp	Val			
	370					375					380							
ggg	gcg	gtg	atc	ccg	gcc	ggg	ttc	gtg	acc	tcg	gca	cac	ggc	aac	gac		1200	
Gly	Ala	Val	Ile	Pro	Ala	Gly	Phe	Val	Thr	Ser	Ala	His	Gly	Asn	Asp			
385					390					395					400			
tac	gcc	gtc	tgg	gag	aag	aac	ggt	gcc	gcg	gca	aca	cta	caa	cgg	agc		1248	
Tyr	Ala	Val	Trp	Glu	Lys	Asn	Gly	Ala	Ala	Ala	Thr	Leu	Gln	Arg	Ser			
				405					410					415				

<210> 88
 <211> 416
 <212> PRT
 <213> Hordeum vulgare

<400> 88

Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
1 5 10 15

Gln Ser Gly Gly Trp Tyr Asn Met Met Met Gly Lys Val Asp Asp Ile
20 25 30

Ala Ala Ala Gly Val Thr His Val Trp Leu Pro Pro Pro Ser His Ser
35 40 45

Val Ser Asn Glu Gly Tyr Met Pro Gly Arg Leu Tyr Asp Ile Asp Ala
50 55 60

Ser Lys Tyr Gly Asn Ala Ala Glu Leu Lys Ser Leu Ile Gly Ala Leu

65

His Gly Lys Gly Val Gln Ala Ile Ala Asp Ile Val Ile Asn His Arg
85 90 95

Cys Ala Asp Tyr Lys Asp Ser Arg Gly Ile Tyr Cys Ile Phe Glu Gly
100 105 110

Gly Thr Ser Asp Gly Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg
115 120 125

Asp Asp Thr Lys Tyr Ser Asp Gly Thr Ala Asn Leu Asp Thr Gly Ala
130 135 140

Asp Phe Ala Ala Ala Pro Asp Ile Asp His Leu Asn Asp Arg Val Gln
145 150 155 160

Arg Glu Leu Lys Glu Trp Leu Leu Trp Leu Lys Ser Asp Leu Gly Phe
165 170 175

Asp Ala Trp Arg Leu Asp Phe Ala Arg Gly Tyr Ser Pro Glu Met Ala
180 185 190

Lys Val Tyr Ile Asp Gly Thr Ser Pro Ser Leu Ala Val Ala Glu Val
195 200 205

Trp Asp Asn Met Ala Thr Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln
210 215 220

Asp Ala His Arg Gln Asn Leu Val Asn Trp Val Asp Lys Val Gly Gly
225 230 235 240

Ala Ala Ser Ala Gly Met Val Phe Asp Phe Thr Thr Lys Gly Ile Leu
245 250 255

Asn Ala Ala Val Glu Gly Glu Leu Trp Arg Leu Ile Asp Pro Gln Gly
260 265 270

Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe
275 280 285

Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro
290 295 300

Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly
305 310 315 320

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp
 325 330 335

Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala
 340 345 350

Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala
 355 360 365

Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val
 370 375 380

Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp
 385 390 395 400

Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Ala Thr Leu Gln Arg Ser
 405 410 415

<210> 89

<211> 1401

<212> DNA

<213> Artificial Sequence

<220>

<223> Trichoderma reesei β -Glucosidase 2

<220>

<221> CDS

<222> (1)..(1401)

<223> Trichoderma reesei β -Glucosidase 2

<400> 89

atg ttg ccc aag gac ttt cag tgg ggg ttc gcc acg gct gcc tac cag 48
 Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
 1 5 10 15

atc gag ggc gcc gtc gac cag gac ggc cgc ggc ccc agc atc tgg gac 96
 Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
 20 25 30

acg ttc tgc gcg cag ccc ggc aag atc gcc gac ggc tcg tcg ggc gtg 144
 Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
 35 40 45

acg gcg tgc gac tcg tac aac cgc acg gcc gag gac att gcg ctg ctg 192
 Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
 50 55 60

aag tcg ctc ggg gcc aag agc tac cgc ttc tcc atc tcg tgg tcg cgc 240
 Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
 65 70 75 80

atc atc ccc gag ggc ggc cgc ggc gat gcc gtc aac cag gcg ggc atc 288
 Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
 85 90 95

60110USPCT1 Corrected SEQ LIST 2-2007.txt

gac Asp	cac His	tac Tyr	gtc Val 100	aag Lys	ttc Phe	gtc Val	gac Asp 105	gac Asp	ctg Leu	ctc Leu	gac Asp	gcc Ala	ggc Gly 110	atc Ile	acg Thr	336
ccc Pro	ttc Phe	atc Ile 115	acc Thr	ctc Leu	ttc Phe	cac His	tgg Trp 120	gac Asp	ctg Leu	ccc Pro	gag Glu	ggc Gly 125	ctg Leu	cat His	cag Gln	384
cgg Arg	tac Tyr 130	ggg Gly	ggg Gly	ctg Leu	ctg Leu	aac Asn 135	cgc Arg	acc Thr	gag Glu	ttc Phe	ccg Pro 140	ctc Leu	gac Asp	ttt Phe	gaa Glu	432
aac Asn 145	tac Tyr	gcc Ala	cgc Arg	gtc Val	atg Met 150	ttc Phe	agg Arg	gcg Ala	ctg Leu	ccc Pro 155	aag Lys	gtg Val	cgc Arg	aac Asn	tgg Trp 160	480
atc Ile	acc Thr	ttc Phe	aac Asn	gag Glu 165	ccg Pro	ctg Leu	tgc Cys	tcg Ser	gcc Ala 170	atc Ile	ccg Pro	ggc Gly	tac Tyr	ggc Gly 175	tcc Ser	528
ggc Gly	acc Thr	ttc Phe	gcc Ala 180	ccc Pro	ggc Gly	cgg Arg	cag Gln	agc Ser 185	acc Thr	tcg Ser	gag Glu	ccg Pro	tgg Trp 190	acc Thr	gtc Val	576
ggc Gly	cac His	aac Asn 195	atc Ile	ctc Leu	gtc Val	gcc Ala	cac His 200	ggc Gly	cgc Arg	gcc Ala	gtc Val	aag Lys 205	gcg Ala	tac Tyr	cgc Arg	624
gac Asp	gac Asp 210	ttc Phe	aag Lys	ccc Pro	gcc Ala	agc Ser 215	ggc Gly	gac Asp	ggc Gly	cag Gln	atc Ile 220	ggc Gly	atc Ile	gtc Val	ctc Leu	672
aac Asn 225	ggc Gly	gac Asp	ttc Phe	acc Thr	tac Tyr 230	ccc Pro	tgg Trp	gac Asp	gcc Ala	gcc Ala 235	gac Asp	ccg Pro	gcc Ala	gac Asp	aag Lys 240	720
gag Glu	gcg Ala	gcc Ala	gag Glu	cgg Arg 245	cgc Arg	ctc Leu	gag Glu	ttc Phe	ttc Phe 250	acg Thr	gcc Ala	tgg Trp	ttc Phe	gcg Ala 255	gac Asp	768
ccc Pro	atc Ile	tac Tyr	ttg Leu 260	ggc Gly	gac Asp	tac Tyr	ccg Pro	gcg Ala 265	tcg Ser	atg Met	cgc Arg	aag Lys	cag Gln 270	ctg Leu	ggc Gly	816
gac Asp	cgg Arg	ctg Leu 275	ccg Pro	acc Thr	ttt Phe	acg Thr	ccc Pro 280	gag Glu	gag Glu	cgc Arg	gcc Ala	ctc Leu 285	gtc Val	cac His	ggc Gly	864
tcc Ser	aac Asn 290	gac Asp	ttt Phe	tac Tyr	ggc Gly	atg Met 295	aac Asn	cac His	tac Tyr	acg Thr	tcc Ser 300	aac Asn	tac Tyr	atc Ile	cgc Arg	912
cac His 305	cgc Arg	agc Ser	tcg Ser	ccc Pro	gcc Ala 310	tcc Ser	gcc Ala	gac Asp	gac Asp	acc Thr 315	gtc Val	ggc Gly	aac Asn	gtc Val	gac Asp 320	960
gtg Val	ctc Leu	ttc Phe	acc Thr	aac Asn 325	aag Lys	cag Gln	ggc Gly	aac Asn	tgc Cys 330	atc Ile	ggc Gly	ccc Pro	gag Glu	acg Thr 335	cag Gln	1008
tcc Ser	ccc Pro	tgg Trp	ctg Leu 340	cgc Arg	ccc Pro	tgt Cys	gcc Ala	gcc Ala 345	ggc Gly	ttc Phe	cgc Arg	gac Asp	ttc Phe 350	ctg Leu	gtg Val	1056

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tgg atc agc aag agg tac ggc tac ccg ccc atc tac gtg acg gag aac	1104
Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn	
355 360 365	
ggc acg agc atc aag ggc gag agc gac ttg ccc aag gag aag att ctc	1152
Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu	
370 375 380	
gaa gat gac ttc agg gtc aag tac tat aac gag tac atc cgt gcc atg	1200
Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met	
385 390 395 400	
gtt acc gcc gtg gag ctg gac ggg gtc aac gtc aag ggg tac ttt gcc	1248
Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala	
405 410 415	
tgg tcg ctc atg gac aac ttt gag tgg gcg gac ggc tac gtg acg agg	1296
Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg	
420 425 430	
ttt ggg gtt acg tat gtg gat tat gag aat ggg cag aag cgg ttc ccc	1344
Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro	
435 440 445	
aag aag agc gca aag agc ttg aag ccg ctg ttt gac gag ctg att gcg	1392
Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala	
450 455 460	
gcg gcg tga	1401
Ala Ala	
465	

<210> 90
 <211> 466
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic Construct

<400> 90

Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
1 5 10 15
Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
20 25 30
Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
35 40 45
Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
50 55 60
Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
65 70 75 80

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
85 90 95

Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
100 105 110

Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
115 120 125

Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
130 135 140

Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp
145 150 155 160

Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser
165 170 175

Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val
180 185 190

Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg
195 200 205

Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu
210 215 220

Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys
225 230 235 240

Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp
245 250 255

Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly
260 265 270

Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly
275 280 285

Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg
290 295 300

His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp
305 310 315 320

Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln
325 330 335

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val
340 345 350

Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn
355 360 365

Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu
370 375 380

Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
385 390 395 400

Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
405 410 415

Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
420 425 430

Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
435 440 445

Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
450 455 460

Ala Ala
465

<210> 91
<211> 2103
<212> DNA
<213> Artificial sequence

<220>
<223> Trichoderma reesei β -Glucosidase D

<220>
<221> CDS
<222> (1)..(2103)
<223> Trichoderma reesei β -Glucosidase D

<400> 91
atg att ctc ggc tgt gaa agc aca ggt gtc atc tct gcc gtc aaa cac 48
Met Ile Leu Gly Cys Glu Ser Thr Gly Val Ile Ser Ala Val Lys His
1 5 10 15

ttt gtc gcc aac gac cag gag cac gag cgg cga gcg gtc gac tgt ctc 96
Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
20 25 30

atc acc cag cgg gct ctc cgg gag gtc tat ctg cga ccc ttc cag atc 144
Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile

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35	40	45	
gta Val	gcc Ala 50	cga Arg	gat Asp
gca Ala	agg Arg	ccc Pro 55	ggc Gly
gca Ala	ttg Leu	atg Met	aca Thr 60
tcc Ser	tac Tyr	aac Asn	aag Lys
192			
gtc Val 65	aat Asn	ggc Gly	aag Lys
cac His	gtc Val 70	gct Ala	gac Asp
agc Ser	gcc Ala	gag Glu 75	ttc Phe
ctt Leu	cag Gln	ggc Gly	att Ile 80
240			
ctc Leu	cgg Arg	act Thr	gag Glu
tgg Trp 85	aat Asn	tgg Trp	gac Asp
cct Pro	ctc Leu 90	att Ile	gtc Val
agc Ser	gac Asp	tgg Trp 95	tac Tyr
288			
ggc Gly	acc Thr	tac Tyr	acc Thr 100
act Thr	att Ile	gat Asp	gcc Ala
atc Ile 105	aaa Lys	gcc Ala	ggc Gly
ctt Leu	gat Asp 110	ctc Leu	gag Glu
336			
atg Met	ccg Pro	ggc Gly 115	gtt Val
tca Ser	cga Arg	tat Tyr	cgc Arg 120
ggc Gly	aaa Lys	tac Tyr	atc Ile
gag Glu 125	tct Ser	gct Ala	ctg Leu
384			
cag Gln 130	gcc Ala	cgt Arg	ttg Leu
ctg Leu	aag Lys	cag Gln 135	tcc Ser
act Thr	atc Ile	gat Asp	gag Glu 140
cgc Arg	gct Ala	cgc Arg	cgc Arg
432			
gtg Val 145	ctc Leu	agg Arg	ttc Phe
gcc Ala	cag Gln 150	aag Lys	gcc Ala
agc Ser	cat His	ctc Leu 155	aag Lys
gtc Val	tcc Ser	gag Glu	gta Val 160
480			
gag Glu	caa Gln	ggc Gly	cgt Arg
gac Asp 165	ttc Phe	cca Pro	gag Glu
gat Asp	cgc Arg 170	gtc Val	ctc Leu
aac Asn	cgt Arg 175	atc Ile	
528			
tgc Cys	ggc Gly	agc Ser	agc Ser 180
att Ile	gtc Val	cta Leu	ctg Leu
aag Lys 185	aat Asn	gag Glu	aac Asn
tcc Ser 190	atc Ile	tta Leu	cct Pro
576			
ctc Leu	ccc Pro	aag Lys 195	tcc Ser
gtc Val	aag Lys	aag Lys	gtc Val 200
gcc Ala	ctt Leu	ggt Gly	tcc Ser 205
624			
cta Leu	ccg Pro	gct Ala	atc Ile
tcg Ser	gga Gly 215	ggc Gly	agc Ser
gcc Ala	tct Ser	ctt Leu 220	gtc Val
cct Pro	tac Tyr	tat Tyr	
672			
gcc Ala 225	ata Ile	tct Ser	cta Leu
gag Glu	gta Val 235	cta Leu	gcc Ala
ggt Gly	gcc Ala	acg Thr 240	
720			
atc Ile	acg Thr	cac His	gag Glu
gtc Val 245	ggc Gly	gcc Ala	tat Tyr
cac His 250	caa Gln	atg Met	ctg Leu
ccc Pro	gtc Val 255	atc Ile	
768			
gac Asp	gca Ala	atg Met	atc Ile 260
agc Ser	aac Asn	gcc Ala	gta Val
atc Ile 265	ttc Phe	tac Tyr	aac Asn
gac Asp 270	ccc Pro	atc Ile	
816			
gat Asp	gtc Val	aaa Lys 275	gac Asp
aga Arg	aag Lys	ctc Leu	ctt Leu 280
ggc Gly	agt Ser	gag Glu	aac Asn
gta Val 285	tcg Ser	tcg Ser	aca Thr
864			
tcg Tyr	ttc Tyr	cag Tyr	ctc Tyr
atg Tyr	gat Tyr	tac Tyr	aac Tyr
912			

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Ser	Phe	Gln	Leu	Met	Asp	Tyr	Asn	Asn	Ile	Pro	Thr	Leu	Asn	Lys	Ala	
290						295					300					
atg	ttc	tgg	ggt	act	ctc	gtg	ggc	gag	ttt	atc	cct	acc	gcc	acg	gga	960
Met	Phe	Trp	Gly	Thr	Leu	Val	Gly	Glu	Phe	Ile	Pro	Thr	Ala	Thr	Gly	
305					310					315					320	
att	tgg	gaa	ttt	ggc	ctc	agt	gtc	ttt	ggc	act	gcc	gac	ctt	tat	att	1008
Ile	Trp	Glu	Phe	Gly	Leu	Ser	Val	Phe	Gly	Thr	Ala	Asp	Leu	Tyr	Ile	
				325					330					335		
gat	aat	gag	ctc	gtg	att	gaa	aat	aca	aca	cat	cag	acg	cgt	gga	acc	1056
Asp	Asn	Glu	Leu	Val	Ile	Glu	Asn	Thr	Thr	His	Gln	Thr	Arg	Gly	Thr	
			340					345					350			
gcc	ttt	ttc	gga	aag	gga	acg	acg	gaa	aaa	gtc	gct	acc	agg	agg	atg	1104
Ala	Phe	Phe	Gly	Lys	Gly	Thr	Thr	Glu	Lys	Val	Ala	Thr	Arg	Arg	Met	
		355					360					365				
gtg	gcc	ggc	agc	acc	tac	aag	ctg	cgt	ctc	gag	ttt	ggg	tct	gcc	aac	1152
Val	Ala	Gly	Ser	Thr	Tyr	Lys	Leu	Arg	Leu	Glu	Phe	Gly	Ser	Ala	Asn	
	370					375					380					
acg	acc	aag	atg	gag	acg	acc	ggt	gtt	gtc	aac	ttt	ggc	ggc	ggt	gcc	1200
Thr	Thr	Lys	Met	Glu	Thr	Thr	Gly	Val	Val	Asn	Phe	Gly	Gly	Gly	Ala	
385					390					395					400	
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Val	His	Leu	Gly	Ala	Cys	Leu	Lys	Val	Asp	Pro	Gln	Glu	Met	Ile	Ala	
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cgg	gcc	gtc	aag	gcc	gca	gcc	gat	gcc	gac	tac	acc	atc	atc	tgc	acg	1296
Arg	Ala	Val	Lys	Ala	Ala	Ala	Asp	Ala	Asp	Tyr	Thr	Ile	Ile	Cys	Thr	
			420					425					430			
gga	ctc	agc	ggc	gag	tgg	gag	tct	gag	ggt	ttt	gac	cgg	cct	cac	atg	1344
Gly	Leu	Ser	Gly	Glu	Trp	Glu	Ser	Glu	Gly	Phe	Asp	Arg	Pro	His	Met	
		435					440					445				
gac	ctg	ccc	cct	ggt	gtg	gac	acc	atg	atc	tcg	caa	gtt	ctt	gac	gcc	1392
Asp	Leu	Pro	Pro	Gly	Val	Asp	Thr	Met	Ile	Ser	Gln	Val	Leu	Asp	Ala	
	450					455					460					
gct	ccc	aat	gct	gta	gtc	gtc	aac	cag	tca	ggc	acc	cca	gtg	aca	atg	1440
Ala	Pro	Asn	Ala	Val	Val	Val	Asn	Gln	Ser	Gly	Thr	Pro	Val	Thr	Met	
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agc	tgg	gct	cat	aaa	gca	aag	gcc	att	gtg	cag	gct	tgg	tat	ggt	ggt	1488
Ser	Trp	Ala	His	Lys	Ala	Lys	Ala	Ile	Val	Gln	Ala	Trp	Tyr	Gly	Gly	
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aac	gag	aca	ggc	cac	gga	atc	tcc	gat	gtg	ctc	ttt	ggc	aac	gtc	aac	1536
Asn	Glu	Thr	Gly	His	Gly	Ile	Ser	Asp	Val	Leu	Phe	Gly	Asn	Val	Asn	
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ccg	tcg	ggg	aaa	ctc	tcc	cta	tcg	tgg	cca	gtc	gat	gtg	aag	cac	aac	1584
Pro	Ser	Gly	Lys	Leu	Ser	Leu	Ser	Trp	Pro	Val	Asp	Val	Lys	His	Asn	
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cca	gca	tat	ctc	aac	tac	gcc	agc	gtt	ggt	gga	cgg	gtc	ttg	tat	ggc	1632
Pro	Ala	Tyr	Leu	Asn	Tyr	Ala	Ser	Val	Gly	Gly	Arg	Val	Leu	Tyr	Gly	
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gtt Val	ctg Leu	ttt Phe	cct Pro	ttt Phe 565	ggg Gly	cat His	ggc Gly	ctg Leu	tct Ser 570	tac Tyr	gct Ala	acc Thr	ttc Phe	aag Lys 575	ctc Leu	1728
cca Pro	gat Asp	tct Ser	acc Thr 580	gtg Val	agg Arg	acg Thr	gtc Val	ccc Pro 585	gaa Glu	acc Thr	ttc Phe	cac His	ccg Pro 590	gac Asp	cag Gln	1776
ccc Pro	aca Thr	gta Val 595	gcc Ala	att Ile	gtc Val	aag Lys	atc Ile 600	aag Lys	aac Asn	acg Thr	agc Ser	agt Ser 605	gtc Val	ccg Pro	ggc Gly	1824
gcc Ala	cag Gln 610	gtc Val	ctg Leu	cag Gln	tta Leu	tac Tyr 615	att Ile	tcg Ser	gcc Ala	cca Pro	aac Asn 620	tcg Ser	cct Pro	aca Thr	cat His	1872
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ttc Phe	tgg Trp	gac Asp	gag Glu 660	att Ile	gag Glu	agc Ser	atg Met	tgg Trp 665	aag Lys	agc Ser	gag Glu	agg Arg	ggc Gly 670	att Ile	tat Tyr	2016
gat Asp	gtg Val	ctt Leu 675	gta Val	gga Gly	ttc Phe	tcg Ser	agt Ser 680	cag Gln	gaa Glu	atc Ile	tcg Ser	ggc Gly 685	aag Lys	ggg Gly	aag Lys	2064
ctg Leu 690	att Ile	gtg Val	cct Pro	gaa Glu	acg Thr	cga Arg 695	ttc Phe	tgg Trp	atg Met	ggg Gly 700	ctg Leu	tag				2103

<210> 92
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 92

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Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
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Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile
 35 40 45

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys
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Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile
 65 70 75 80

Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr
 85 90 95

Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu
 100 105 110

Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu
 115 120 125

Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg
 130 135 140

Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val
 145 150 155 160

Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile
 165 170 175

Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro
 180 185 190

Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg
 195 200 205

Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr
 210 215 220

Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr
 225 230 235 240

Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile
 245 250 255

Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile
 260 265 270

Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr
 275 280 285

Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala
 290 295 300

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
305 310 315 320

Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
325 330 335

Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr
340 345 350

Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
355 360 365

Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
370 375 380

Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
385 390 395 400

Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
405 410 415

Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
420 425 430

Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
435 440 445

Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
450 455 460

Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
465 470 475 480

Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
485 490 495

Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
500 505 510

Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
515 520 525

Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
530 535 540

Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
545 550 555 560

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
565 570 575

Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
580 585 590

Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
595 600 605

Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
610 615 620

Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
625 630 635 640

Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
645 650 655

Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly Ile Tyr
660 665 670

Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
675 680 685

Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
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<211> 1496
<212> DNA
<213> Artificial Sequence

<220>
<223> Maize optimized CBHI

<400> 93
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ggacccacgc caccaactcc tccaccaact gctacgacgg caacacctgg tcctccaccc 180
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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ccatctccga	ggccctcacc	ccgcacccgt	gcaccaccgt	gggccaggag	atctgcgagg	720
gcgacggctg	cggcggcacc	tactccgaca	accgctacgg	cggcacctgc	gacccggacg	780
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<210> 94

<211> 1365

<212> DNA

<213> Artificial Sequence

<220>

<223> Maize optimized CBHII

<400> 94

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accgccaaca	agaacggcgg	caactacgcc	ggccagtctg	tggtgtacga	cctcccggac	540
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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aagtgcgcca acgcccagtc cgcctacctc gagtgcatac actacgccgt gaccagctc 780
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<210> 95

<211> 1317

<212> DNA

<213> Artificial Sequence

<220>

<223> Maize optimized EGLI

<400> 95

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tcctgcaccc	agaccactg	gggccagtgc	ggcggcatcg	gctactccgg	ctgcaagacc	1260
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<210> 96

<211> 1401

<212> DNA

<213> Artificial Sequence

<220>

<223> Maize optimized BGLII

<400> 96

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 tag 2103

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 <211> 420
 <212> DNA
 <213> Zea mays

<220>
 <223> Q protein promoter

<400> 98
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 ctagtgtgca caagttgtat atcgattcgt cgcgtttcaa caactcatgc aacattacaa 120
 acaagtaaca caatattaca aagttagttt catacaaagc aagaaaagga caataatact 180
 tgacatgtaa agtgaagctt attatacttc ctaatccaac acaaaacaaa aaaaagttgc 240
 acaaagggtcc aaaaatccac atcaaccatt aacctatacg taaagtgagt gatgagtcac 300
 attatccaac aaatgtttat caatgtggta tcatacaagc attgacatcc cataaatgca 360
 agaaattgtg ccaacaaagc tataagtaac cctcatatgt atttgcactc atgcatcaca 420

<210> 99
 <211> 1188
 <212> DNA
 <213> artificial sequence

<220>

<223> synthetic ferulic acid esterase

<400> 99

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ccgcgcggcc aggtggtgaa catctcctac ttctccaccg ccaccaactc caccgccccg      120
gcccgcggtg acctcccgcc gggctactcc aaggacaaga agtactccgt gctctacctc      180
ctccacggca tcggcggctc cgagaacgac tggttcgagg gcggcggccg cgccaacgtg      240
atcgccgaca acctcatcgc cgagggcaag atcaagccgc tcatcatcgt gaccccgaac      300
accaacgccg ccggccccggg catcgccgac ggctacgaga acttcaccaa ggacctcctc      360
aactccctca tcccgtagat cgagtccaac tactccgtgt acaccgaccg cgagcaccgc      420
gccatcgccg gcctctctat gggcggcggc cagtccttca acatcggcct caccaacctc      480
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ctcttccccg acggcggcaa ggccgccccg gagaagctca agctcctctt catcgcctgc      600
ggcaccaacg actccctcat cggcttcggc cagcgcgtgc acgagtactg cgtggccaac      660
aacatcaacc acgtgtactg gctcatccag ggcggcggcc acgacttcaa cgtgtggaag      720
ccgggcctct ggaacttcct ccagatggcc gacgaggccg gcctcaccg cgacggcaac      780
accccggtgc cgaccccgtc cccgaagccg gccaacaccc gcatcgaggc cgaggactac      840
gacggcatca actcctcctc catcgagatc atcggcgtgc cgccggaggg cggccgcggc      900
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gccacctcct tcaaggccaa ggtggccaac gccaacacct ccaacatcga gcttcgcctc     1020
aacggccccg acggcaccct catcggcacc ctctccgtga agtccaccg cgactggaac     1080
acctacgagg agcagacctg ctccatctcc aaggtgaccg gcatcaacga cctctacctc     1140
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<210> 100

<211> 395

<212> PRT

<213> artificial sequence

<220>

<223> synthetic ferulic acid esterase

<400> 100

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Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val
1           5           10           15

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```

Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
20           25           30

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```

Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly

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35

40

45

Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
50 55 60

Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
65 70 75 80

Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
85 90 95

Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
100 105 110

Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
115 120 125

Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
130 135 140

Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
145 150 155 160

Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
165 170 175

Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
180 185 190

Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
195 200 205

Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
210 215 220

Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
225 230 235 240

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
275 280 285

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
385 390 395

<210> 101
<211> 1188
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13036

<400> 101
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ccgcgcggcc aggtggtgaa catctcctac ttctccaccg ccaccaactc caccgcccg 120
gcccgcgtgt acctcccgcc gggctactcc aaggacaaga agtactccgt gctctacctc 180
ctccacggca tcggcggctc cgagaacgac tggttcgagg gcggcggccg cgccaacgtg 240
atcgccgaca acctcatcgc cgagggcaag atcaagccgc tcatcatcgt gaccccgaac 300
accaacgccg ccggcccggg catcgccgac ggctacgaga acttcaccaa ggacctctc 360
aactccctca tcccgtacat cgagtccaac tactccgtgt acaccgaccg cgagcaccgc 420
gccatcgccg gcctctctat gggcggcggc cagtccttca acatcggcct caccaacctc 480
gacaagttcg cctacatcgg cccgatctcc gccgccccga acacctacc gaacgagcgc 540
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ggcaccaacg actccctcat cggcttcggc cagcgcgtgc acgagtactg cgtggccaac 660
aacatcaacc acgtgtactg gctcatccag ggcggcggcc acgacttcaa cgtgtggaag 720
ccgggcctct ggaacttcct ccagatggcc gacgaggccg gcctcaccg cgacggcaac 780

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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 gccacctcct tcaaggccaa ggtggccaac gccaacacct ccaacatcga gcttcgcctc 1020
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 acctacgagg agcagacctg ctccatctcc aaggtgaccg gcatcaacga cctctacctc 1140
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<210> 102
 <211> 395
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13036

<400> 102

Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val
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Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
20 25 30

Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly
35 40 45

Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
50 55 60

Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
65 70 75 80

Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
85 90 95

Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
100 105 110

Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
115 120 125

Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
130 135 140

Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
145 150 155 160

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
165 170 175

Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
180 185 190

Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
195 200 205

Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
210 215 220

Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
225 230 235 240

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
275 280 285

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
385 390 395

<210> 103

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<211> 1245
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 13038

<400> 103
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 gccgcctccc tcccgaccat gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120
 cgcggccagg tggatgaacat ctctacttcc tccaccgcca ccaactccac ccgcccggcc 180
 cgcggtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctcctc 240
 cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300
 gccgacaacc tcacgcccga gggcaagatc aagccgctca tcacgtgac cccgaacacc 360
 aacgccgccg gcccgggcat cgccgacggc tacgagaact tcaccaagga cctcctcaac 420
 tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 480
 atcgccggcc tctctatggg cggcgggccag tccttcaaca tcggcctcac caacctcgac 540
 aagttcgcct acatcgggcc gatctccgcc gcccgaaca cctacccgaa cgagcgcctc 600
 ttcccggacg gcggcaaggc cgcccgcgag aagctcaagc tcctcttcat cgcctgcggc 660
 accaacgact ccctcatcgg cttcggccag cgcggtgcac agtactgcgt ggccaacaac 720
 atcaaccacg tgtactggct catccagggc ggcgggccac acttcaacgt gtggaagccg 780
 ggcctctgga acttcctcca gatggccgac gaggccggcc tcacccgcga cggcaacacc 840
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 ggcatcaact cctcctccat cgagatcatc ggcggtgccg cgaggggcgg ccgcggcatc 960
 ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc 1020
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<210> 104
 <211> 414
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13038 aa

<400> 104

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20 25 30

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35 40 45

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50 55 60

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65 70 75 80

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
85 90 95

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
100 105 110

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
115 120 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
130 135 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
145 150 155 160

Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
165 170 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
180 185 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
195 200 205

Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
210 215 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
225 230 235 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
245 250 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala

260

265

270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
275 280 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
340 345 350

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
405 410

<210> 105
<211> 1425
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13039

<400> 105
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gacgcgtcca cgttccgccg cggcgccgcg cagggcctga ggggggcccg ggcgtcggcg 120
gcggcggaca cgctcagcat gcggaccagc gcgcgcgcgg cgcccaggca ccagcaccag 180
caggcgcgcc gcggggccag gttcccgtcg ctgctcgtgt gcgccagcgc cggcgccatg 240
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cgcggccagg tgggtgaacat ctctacttc tccaccgcca ccaactccac ccgcccggcc 360
cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctctc 420
cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 480

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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aacgccgccg gcccgggcat cgccgacggc tacgagaact tcaccaagga cctcctcaac 600
tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcca gcaccgccc 660
atcgccggcc tctctatggg cggcggccag tccttcaaca tcggcctcac caacctcgac 720
aagttcgctt acatcggccc gatctccgcc gccccgaaca cctacccgaa cgagcgcttc 780
ttcccggacg gcggcaaggc cgcccgcgag aagctcaagc tcctcttcat cgcctgcggc 840
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atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 960
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acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1260
ggcccgaacg gcaccctcat cggcaccttc tccgtgaagt ccaccggcca ctggaacacc 1320
tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg 1380
ttcaagggcc cgggtgaacat cgactgggtc accttcggcg tgtag 1425

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<210> 106
 <211> 474
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13039 aa

<400> 106

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
 1 5 10 15

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
 20 25 30

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
 35 40 45

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
 50 55 60

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
 65 70 75 80

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val Arg
85 90 95

Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser Thr
100 105 110

Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly Tyr
115 120 125

Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile Gly
130 135 140

Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val Ile
145 150 155 160

Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile Val
165 170 175

Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr Glu
180 185 190

Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu Ser
195 200 205

Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly Leu
210 215 220

Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu Asp
225 230 235 240

Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr Pro
245 250 255

Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys Leu
260 265 270

Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly Phe
275 280 285

Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His Val
290 295 300

Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys Pro
305 310 315 320

Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr Arg
325 330 335

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn Thr
340 345 350

Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile Glu
355 360 365

Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile Thr
370 375 380

Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly Ala
385 390 395 400

Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile Glu
405 410 415

Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser Val
420 425 430

Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser Ile
435 440 445

Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly Pro
450 455 460

Val Asn Ile Asp Trp Phe Thr Phe Gly Val
465 470

<210> 107
<211> 1263
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13347

<400> 107
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gccgcctccc tcccgaccat gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120
cgcggccagg tgggtgaacat ctctacttc tccaccgcca ccaactccac ccgcccggcc 180
cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctctc 240
cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300
gccgacaacc tcatcgccga gggcaagatc aagccgctca tcatcgtgac cccgaacacc 360
aacgccgccg gcccgggcat cgccgacggc tacgagaact tcaccaagga cctcctcaac 420
tcctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 480

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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 aagttcgctt acatcggccc gatctccgcc gccccgaaca cctacccgaa cgagcgctc 600
 ttcccggacg gcggcaaggc cgcccgcgag aagctcaagc tcctcttcat cgcctgcggc 660
 accaacgact ccctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac 720
 atcaaccacg tgtactggct catccagggc ggcgggccacg acttcaacgt gtggaagccg 780
 ggcttctgga acttctcca gatggccgac gaggccggcc tcacccgcga cggcaacacc 840
 ccggtgccga ccccgctccc gaagccggcc aacacccgca tcgaggccga ggactacgac 900
 ggcatcaact cctcctccat cgagatcatc ggcggtgccg cggagggcgg ccgcggcatc 960
 ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc 1020
 acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1080
 ggcccgaacg gcacctcat cggcaccctc tccgtgaagt ccaccggcga ctggaacacc 1140
 tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg 1200
 ttcaagggcc cggtgaacat cgactggttc accttcggcg tgtccgagaa ggacgaactc 1260
 tag 1263

<210> 108
 <211> 420
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13347

<400> 108

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20 25 30

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35 40 45

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50 55 60

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65 70 75 80

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
85 90 95

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
 100 105 110

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
 115 120 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
 130 135 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
 145 150 155 160

Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
 165 170 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
 180 185 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
 195 200 205

Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
 210 215 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
 225 230 235 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
 245 250 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
 260 265 270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
 275 280 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
 290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
 305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
 325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
 340 345 350

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Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val Ser Glu
405 410 415

Lys Asp Glu Leu
420

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<213> artificial sequence

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cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccgagcgc ctggccgacc 180
tggccggtga agctcggcga gctgaccccg cgcggcggcg agctgatcgc ctacctcggc 240
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tccggccagg tggccatcat cgccgacgtg gacgagcgca cccgcaagac cggcgaggcc 360
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tccccggacc cgctcttcaa cccgctcaag accggcgtgt gccagctcga caacgccaac 480
gtgaccgacg ccattcctgga gcgcgcccgc ggctccatcg ccgacttcac cggccactac 540
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accccgcacc cgccgcagaa gcaggcctac ggcgtgaccc tcccagacct cgtgctcttc 960
atcgccggcc acgacaccaa cctcgccaac ctcggcggcg ccctggagct gaactggacc 1020

60110USPCT1 Corrected SEQ LIST 2-2007.txt

ctcccggggcc agccggacaa caccgccg ggcggcgagc tgggtgttcga gcgctggcgc 1080
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 atgcgcgaca agaccccgct ctccctcaac accccgccgg gcgaggtgaa gctcaccctc 1200
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 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 11267 aa sequence

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Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
 20 25 30

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
 35 40 45

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
 50 55 60

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
 65 70 75 80

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
 85 90 95

Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
 100 105 110

Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
 115 120 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
 130 135 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
 145 150 155 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
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Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
225 230 235 240

Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
245 250 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
260 265 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
275 280 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
290 295 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
405 410 415

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 11268

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 tggccggtga agctcggcga gctgaccccg cgcggcggcg agctgatcgc ctacctcggc 240
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 tccggccagg tggccatcat cgccgacgtg gacgagcgca cccgcaagac cggcgaggcc 360
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 aagcgcgaga agcaggacga gtcctgctcc ctcacccagg ccctcccgtc cgagctgaag 660
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 tcccaccagt ggaacaccct cctctccctc cacaacgccc agttcgacct cctccagcgc 840
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>

<223> plasmid 11268 amino acid sequence

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Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
20 25 30

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
35 40 45

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
50 55 60

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
65 70 75 80

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
85 90 95

Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
100 105 110

Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
115 120 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
130 135 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
145 150 155 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
165 170 175

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
225 230 235 240

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
245 250 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
260 265 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
275 280 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
290 295 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
405 410 415

Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu Ser
420 425 430

Glu Lys Asp Glu Leu
435